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OM protein - protein search, using sw model

Run on: February 2, 2004, 14:21:01 ; Search time 22 Seconds
(without alignments)
434.648 Million cell updates/sec

Title: US-09-965-529-26

Perfect score: 1200

Sequence: 1 MKMVAAPTRFYNSCCILCCH.....YDDATYNGAAKEPPPPVSA 226

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Scoring table: 328717 seqs, 42310858 residues

Searched: Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgns_6/patdata/1/1aa/5A_COMB.pep:*

2: /cgns_6/patdata/1/1aa/5B_COMB.pep:*

3: /cgns_6/patdata/1/1aa/6A_COMB.pep:*

4: /cgns_6/patdata/1/1aa/6B_COMB.pep:*

5: /cgns_6/patdata/1/1aa/PCUTS_COMB.pep:*

6: /cgns_6/patdata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	769	64.1	162	4	US-09-152-060-63	Sequence 63, App1
2	714	59.5	137	4	US-09-152-060-97	Sequence 97, App1
3	553.5	46.1	233	4	US-09-088-319A-12	Sequence 12, App1
4	541.5	45.1	233	4	US-09-088-319A-11	Sequence 11, App1
5	417	34.8	87	4	US-09-052-060-98	Sequence 98, App1
6	175.5	14.6	262	3	US-08-088-425-2	Sequence 2, App1
7	156	11.0	261	3	US-08-088-425-4	Sequence 4, App1
8	95	7.9	1872	6	5386025-6	Patent No. 5386025
9	95	7.9	1873	1	US-08-435-675B-4	Sequence 4, App1
10	95	7.9	1873	1	US-08-436-257A-7	Sequence 7, App1
11	89	7.4	713	4	US-09-07-532A-1559	Sequence 4559, App1
12	88.5	7.4	2161	1	US-07-745-206A-2	Sequence 2, App1
13	88.5	7.4	2161	1	US-08-455-543A-49	Sequence 49, App1
14	88.5	7.4	2161	1	US-08-455-543A-51	Sequence 51, App1
15	88.5	7.4	2161	2	US-08-223-305C-49	Sequence 49, App1
16	88.5	7.4	2161	2	US-08-223-305C-51	Sequence 2, App1
17	88.5	7.4	2161	2	US-08-11-363-2	Sequence 2, App1
18	87.5	7.3	451	1	US-08-191-137-3	Sequence 3, App1
19	87.5	7.3	548	4	US-09-328-352-6605	Sequence 6605, App1
20	86.5	7.2	241	4	US-09-07-532A-5558	Sequence 5558, App1
21	85.5	7.1	667	3	US-08-059-004-11	Sequence 11, App1
22	83	6.9	775	4	US-09-25-991A-2844	Sequence 28461, App1
23	83	6.9	870	4	US-09-134-001C-1959	Sequence 4959, App1
24	82.5	6.9	493	3	US-08-476-123-12	Sequence 12, App1
25	80	6.7	315	4	US-09-393-64-56	Sequence 56, App1
26	80	6.7	1968	7	US-07-206A-7	Sequence 7, App1
27	80	6.7	1968	1	US-08-455-543A-45	Sequence 45, App1

ALIGNMENTS

RESULT 1
US-09-152-060-63
; Sequence 63, Application US/09152060
; Patent No. 6448230
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P1.US
; CURRENT APPLICATION NUMBER: US/09/152,060
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER APPLICATION DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER APPLICATION DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER APPLICATION DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
; EARLIER APPLICATION DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100
; EARLIER APPLICATION DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER APPLICATION DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER APPLICATION DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER APPLICATION DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER APPLICATION DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER APPLICATION DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 63
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-152-060-63

Qy 1 MKMVPWTRFYNSCCCLCCCHVRGTVLGLGWLILSALADPQYNFSSSEL 60
Db 1 MKMVPWTRFYNSCCCLCCCHVRGTVLGLGWLILSALADPQYNFSSSEL 60

Qy 61 GGDFEFMDDDANMCIAIAISLMLICAMATYGAAYKQRAAWIIPFCYQIFDFALNLVAI 120
Db 61 GGDFEFMDDDANMCIAIAISLMLICAMATYGAAYKQRAAGIIPFCYQIFDFALNLVAI 120

RESULT 2
 US-09-152-06-0-97
 ; Sequence 97, Application US/09152060,
 ; Patent No. 6448230
 ; GENERAL INFORMATION:
 ; TITLE OF INVENTION: 28 Human Secreted Proteins
 ; FILE REFERENCE: P200321.US
 ; CURRENT APPLICATION NUMBER: US/09/152,060
 ; CURRENT FILING DATE: 1998-09-11
 ; EARLIER APPLICATION NUMBER: PCT/US98/048358
 ; EARLIER FILING DATE: 1998-03-12
 ; EARLIER APPLICATION NUMBER: 60/040,762
 ; EARLIER FILING DATE: 1997-03-14
 ; EARLIER APPLICATION NUMBER: 60/040,710
 ; EARLIER FILING DATE: 1997-03-14
 ; EARLIER APPLICATION NUMBER: 60/050,934
 ; EARLIER FILING DATE: 1997-05-30
 ; EARLIER APPLICATION NUMBER: 60/048,100
 ; EARLIER FILING DATE: 1997-05-30
 ; EARLIER APPLICATION NUMBER: 60/048,357
 ; EARLIER FILING DATE: 1997-05-30
 ; EARLIER APPLICATION NUMBER: 60/048,189
 ; EARLIER FILING DATE: 1997-05-30
 ; EARLIER APPLICATION NUMBER: 60/057,765
 ; EARLIER FILING DATE: 1997-09-05
 ; EARLIER APPLICATION NUMBER: 60/048,970
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/068,368
 ; EARLIER FILING DATE: 1997-12-19
 ; NUMBER OF SEQ ID NOS: 118
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 97
 ; LENGTH: 137
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-152-06-0-97

Query Match 59 5%; Score 714; DB 4; Length 137;
 Best Local Similarity 99.3%; Pred. No. 4.2e-68;
 Matches 136; Conservative 0; Gaps 0;

Qy 9 RFSNSCCCLCCHVTRGTTLGVWLLNAVLLLILSALADPQYNFSSSELGGDFEFD 68
 Db 1 RFSNSCCCLCCHVTRGTTLGVWLLNAVLLLILSALADPQYNFSSSELGGDFEFD 60

Qy 69 DANMCTAATSLMLIICANATGAYKQRAAWITFFCYQIFDFALNMVAITVLYPNS 128
 Db 61 DANMCTAATSLMLIICANATGAYKQRAAGIIPFCQIFDFALNMVAITVLYPNS 120

Qy 129 IQEYIRQLPPNFPYRDD 145
 Db 121 IQEYIRQLPPNFPYRDD 137

RESULT 3
 US-09-886-319A-12
 ; Sequence 12, Application US/09886319A
 ; GENERAL INFORMATION:
 ; Patent No. 6586185
 ; APPLICANT: Wolf, Eckard
 ; APPLICANT: Werner, Sabine
 ; APPLICANT: Halle, Jorn-Peter
 ; APPLICANT: Regenbogen, Johannes
 ; APPLICANT: Goppelt, Andreas
 ; TITLE OF INVENTION: Use of Polypeptides or Nucleic Acids for
 ; TITLE OF INVENTION: the Diagnosis or Treatment of Skin Disorders and Wound
 ; TITLE OF INVENTION: Healing and for the Identification of Pharmacologically

; TITLE OF INVENTION: Active Substances
 ; FILE REFERENCE: 50125/014002
 ; CURRENT APPLICATION NUMBER: US/09/886,319A
 ; CURRENT FILING DATE: 2001-06-20
 ; PRIOR APPLICATION NUMBER: US 60/222,081
 ; PRIOR FILING DATE: 2000-08-01
 ; PRIOR APPLICATION NUMBER: DE 10030149.5
 ; PRIOR FILING DATE: 2000-06-20
 ; NUMBER OF SEQ ID NOS: 84
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 12
 ; LENGTH: 233
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-886-319A-12

Query Match 46.1%; Score 553.5; DB 4; Length 233;
 Best Local Similarity 45.2%; Pred. No. 7.8e-51;
 Matches 104; Conservative 45; Mismatches 60; Indels 21; Gaps 6;

Qy 9 RFSNSCCCLCCHVTRGTTLGVWLLNAVLLLILSALADPQY---QY---NFSS 57
 Db 13 RFSNSCCCLCCHVTRGTTLGVWLLNAVLLLILSALADPQY---QY---NFSS 57

Qy 58 SELGGDFEFDANMCTAATSLMLIICANATGAYKQRAAWITFFCYQIFDFALNM 117
 Db 73 SERMAD-----NAVCLPASVNMFISSMLVGAISYQVGWLIPIFFCYRLFDVLSC 125

Qy 118 VAITYLIVPNSIQBYIQLRQLPPNFPYRDDVMSVNPCTCLVLLFISIILTFKGYLVSCW 177
 Db 126 VAISSTLVLPRIKEYDQL-PDFYKDDILALDSSCLLFLVYFALFLFIFKAYLINCWV 184

Qy 178 NCYTYINGRNSSDVLY-VTSNDTTLVLPYDATTNGAAKEPPPVSA 226
 Db 185 NCYKXINNRRNVPETAVYPAFEAPPQVLPYEMA-VKRMPEKEFPPPYLPA 233

RESULT 4
 US-09-886-319A-11
 ; Sequence 11, Application US/09886319A
 ; Patent No. 6586185
 ; GENERAL INFORMATION:
 ; APPLICANT: Wolf, Eckard
 ; APPLICANT: Werner, Sabine
 ; APPLICANT: Halle, Jorn-Peter
 ; APPLICANT: Regenbogen, Johannes
 ; APPLICANT: Goppelt, Andreas
 ; TITLE OF INVENTION: Use of Polypeptides or Nucleic Acids for
 ; TITLE OF INVENTION: the Diagnosis or Treatment of Skin Disorders and Wound
 ; TITLE OF INVENTION: Healing and for the Identification of Pharmacologically
 ; TITLE OF INVENTION: Active Substances
 ; FILE REFERENCE: 50125/014002
 ; CURRENT APPLICATION NUMBER: US/09/886,319A
 ; CURRENT FILING DATE: 2001-06-20
 ; PRIOR APPLICATION NUMBER: US 60/222,081
 ; PRIOR FILING DATE: 2000-08-01
 ; PRIOR APPLICATION NUMBER: DE 10030149.5
 ; NUMBER OF SEQ ID NOS: 84
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 11
 ; LENGTH: 233
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-886-319A-11

Query Match 45.1%; Score 541.5; DB 4; Length 233;
 Best Local Similarity 44.8%; Pred. No. 1.5e-49;
 Matches 103; Conservative 44; Mismatches 62; Indels 21; Gaps 6;

Qy 9 RFSNSCCCLCCHVTRGTTLGVWLLNAVLLLILSALADPQY---QY---NFSS 57
 Db 13 RFSNSCCCLCCHVTRGTTLGVWLLNAVLLLILSALADPQY---QY---NFSS 57

58 SELGGDFEFNDAMCIAAISLAMILICAMATYGAYKORAATIIPFFCYQIIPDFALANM 117
 73 SERMAD-----NACVLPAVSVLMPPIIISMLVGAISQVGWLIPPFCTRLDFVLSC 125
 118 VAITVLIYPPNSIOEYIROLPPNPYPRDDMSVNPTCLVLVILIPISIILTFKGYLISCW 177
 126 VAISLTYLDRIKEYLDQL-PDFPYKDDLLADQLSSCLLIVLVEFVFLIFRAYLINCW 184
 178 NCYRYTNGNSSDVLY-TTSNDTIVLLEPYDDATVNGAAKEPPPPYSA 226.
 185 NCYKYNRNRVPEAVYPAFETPPQYVLPYEMA-VKIEKEPPPPYLP 233

RESULT 5
 US-09-152-060-98
 Sequence 98, Application US/09152060
 Patent No. 6448230
 GENERAL INFORMATION:
 APPLICANT: Rosen et al.
 TITLE OF INVENTION: 28 Human Secreted Proteins
 FILE REFERENCE: PZ001PL US
 CURRENT APPLICATION NUMBER: US/09/152,060
 CURRENT FILING DATE: 1998-09-11
 EARLIER APPLICATION NUMBER: PCT/US98/04858
 EARLIER FILING DATE: 1998-03-12
 EARLIER APPLICATION NUMBER: 60/040,762
 EARLIER FILING DATE: 1997-03-14
 EARLIER APPLICATION NUMBER: 60/040,710
 EARLIER FILING DATE: 1997-03-14
 EARLIER APPLICATION NUMBER: 60/050,934
 EARLIER FILING DATE: 1997-05-30
 EARLIER APPLICATION NUMBER: 60/048,100
 EARLIER FILING DATE: 1997-05-30
 EARLIER APPLICATION NUMBER: 60/048,357
 EARLIER FILING DATE: 1997-05-30
 EARLIER APPLICATION NUMBER: 60/048,189
 EARLIER FILING DATE: 1997-05-30
 EARLIER APPLICATION NUMBER: 60/057,765
 EARLIER FILING DATE: 1997-09-05
 EARLIER APPLICATION NUMBER: 60/048,970
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/068,368
 EARLIER FILING DATE: 1997-12-19
 NUMBER OF SEQ ID NOS: 118
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO: 98
 LENGTH: 87
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-152-060-98
 1 PPTEMSCAVNPTCLVLILFISILTFKGYLISCVWNCTRYINGRNSSDVLYVTSND 60

Query Match Score 417; DB 4; Length 87;
 Best Local Similarity 92.0%; Pred. No. 6.4e-37;
 Matches 80; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

200 TTVLPPYDDATVNGAAKEPPPPYSA 226
 61 TTVLPPYDDATVNGAAKEPPPPYSA 87

RESULT 6
 US-08-889-425-2
 Sequence 2, Application US/08889425
 Patent No. 6153403
 GENERAL INFORMATION:
 APPLICANT: Bing
 APPLICANT: Adra, Chaker N.
 TITLE OF INVENTION: A Lysosomal-Associated Multispanning

Membrane Protein, LAPTM5 and a Nucleic Acid Encoding
 TITLE OF INVENTION: Membrane Protein, LAPTM5
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 STREET: Two Militia Drive
 CITY: Lexington
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02173
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/889,425
 FILING DATE: 08-JUL-1997
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Brook, David E.
 REGISTRATION NUMBER: 22,592
 REFERENCE/DOCKET NUMBER: BIH96-09DA
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (781) 861-6240
 TELEFAX: (781) 861-9540
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 262 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-889-425-2

Query Match Score 175.5; DB 3; Length 262;
 Best Local Similarity 22.8%; Pred. No. 9.1e-11;
 Matches 61; Conservative 48; Mismatches 83; Indels 75; Gaps 12;

Qy 14 SCCLCHVRTGTTILGVWYLIINAVVLLILSALADPDDYNNFSSSELGGDFEFMDANNC 73
 Db 11 TCC-CFENRVIATTALAIYHVIM-SVLLFTEHSVEAHGKASCKLSQMG---YLRADIIL 64
 Qy 74 IAIASLMLICAMATYGAYKORAATIIPFFCYQIIFPALNMLVAVTLYPNISIOBYI 133
 Db 65 SSPLILTMFIISLSSLIGVVKQREKYLIPFLSQUIMDYLCLLTLGGYI---ELPAYL 121
 Qy 134 ---RQLPPNFPYR----DDVMSVNPTC----- 153
 Db 122 KLASRBRASSSKFKPMTLQLLDFCISILTLCSSTMVEPTYLNFKSMNHMNLYLPSQEDMPH 181
 Qy 154 -----LVIILLLFISIILTFKGYLISCVWNCTRYINGRNS 201
 Db 182 NQFIKMMIFSIASIAFTVLI-FKVMFKCTWRCKMNSVEBKRN5KML-----QK 233
 RESULT 7
 US-08-889-425-4
 Sequence 4, Application US/08889425
 Patent No. 6153403
 GENERAL INFORMATION:
 APPLICANT: Bing
 APPLICANT: Adra, Chaker N.
 TITLE OF INVENTION: A Lysosomal-Associated Multispanning
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 STREET: Two Militia Drive

CITY: Lexington
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02173
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/889,425
 FILING DATE: 08-JUL-1997
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Brook, David E.
 REGISTRATION NUMBER: 22,592
 TELECOMMUNICATION INFORMATION: B1H96-09PA
 TELEPHONE: (781) 861-6240
 TELEFAX: (781) 861-9540
 SEQUENCE CHARACTERISTICS:
 LENGTH: 261 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-889-425-4

Query Match 13.0%; Score 156; DB 3; Length 261;
 Best Local Similarity 22.4%; Pred. No. 1.1e-08;
 Matches 60; Conservative 48; Mismatches 82; Indels 78; Gaps 13;

Qy 14 SCCLCCHVRYGTCILIGWVYLJINAVVLLILSALADPQDNFSSSEBLGGDFEPMDDANIC 73
 Db 11 TCC-CPNIRVATLAIYHIVMS--VLLTEHVV----EVARGKVSRCFKPYLRA 61

Qy 74 IAIATSL--MILICAMATYGAYKORAAWLIIPFFCYQIFDPALMLVAITVLYPNSQ 130
 Db 62 DLLSSPLIGLFLTISLISLFGWVKNREKYLIPFFSLQIMDFLLCLLTGYSI--ELP 118

Qy 131 EYIRQLPNN-FPYRDDVMSN--PTCLVLILL----- 160
 Db 119 AYLKLARPPOPSSKPYLMQLQDLCFLSILTLCSSYMEPTYLNFKSMHNMNLPSEQGV 178

Qy 161 ---FISLITF-----KGYLISCVNCCRYINGNSSDVLYVTSNDT---- 201
 Db 179 PHSQFINNMFLIFSVAFITVLLKVMFKCYTCFLKHMNSA-----MEDSSKML 231

Qy 202 -VLLPPYDADTNGAAKEP-----PPY 223
 Db 232 KVALPSYEAL-SLSPFPKTPESDPAPPY 258

RESULT 8
 5386025-6
 Patent No. 5386025
 APPLICANT: JAY, SCOTT D.; ELLIS, STEVEN B.; HARPOLD, MICHAEL
 M.; CAMPBELL, KEVIN P.
 TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS
 NUMBER OF SEQUENCES: 9
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/482,384
 FILING DATE: 20-FEB-1990
 SEQ ID NO: 6;
 LENGTH: 1872

Query Match 7.9%; Score 95; DB 6; Length 1872;
 Best Local Similarity 24.0%; Pred. No. 0.35;
 Matches 46; Conservative 31; Mismatches 69; Indels 46; Gaps 9;

Qy 12 SNSCCLCCHVRTGTLGWLGYLLIAVVLILLSSA---DPDQYNNFSSSELGDFEPM 67

Db 785 TNKVRVLCH---RIVNATWF--TNFILLFILLSSAALAAEDPIRAESVRNQILGYFD-- 836
 Qy 68 DDANNMCIATAISLMLIGAMATYGAYKORAAWLIIPFFCYQIFDPALMLVAITVLYPNS 127
 Db 837 -----IAFTSVFTEVILKMTYGAFLHKG-----FCRNFYNI-LDILVVAVSLI-- 881
 Qy 128 SIQEYIRQLPNNFPYRDDVMSVNPCTCLVLLPISIILTPKG--YLISCVNCCRYING 185
 Db 882 -----SMGLESSISVVKLRLVRLPRLRAKGLKHHVQCVFVALRTGN 930
 Qy 186 RNSSPVLVYVTS 197
 Db 931 -----IVLVTT 936

RESULT 9
 US-08-435-675B-4
 Sequence 4; Application US/08435675B
 GENERAL INFORMATION:
 / APPLICANT: ELLIS, Steven Bradley
 / APPLICANT: Williams, Mark E.
 / APPLICANT: Harpold, Michael Miller
 / APPLICANT: Schwartz, Arnold
 / APPLICANT: Brenner, Robert
 TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Brown, Martin, Haller & McClain
 STREET: 1660 Union Street
 CITY: San Diego
 STATE: CA
 COUNTRY: USA
 ZIP: 92101-2926
 COMPUTER READABLE FORM:
 COMPUTER TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/435,675B
 FILING DATE: 05-MAY-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/314,083
 FILING DATE: 28-SEP-1994
 APPLICATION NUMBER: US 07/914,231
 FILING DATE: 13-JUL-1992
 APPLICATION NUMBER: US 07/603,751
 FILING DATE: 08-NOV-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Seidman, Stephanie L
 REGISTRATION NUMBER: 33,779
 REFERENCE/DOCKET NUMBER: 63362-53193
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-238-0062
 TELEFAX: 619-238-0999
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1873 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 US-08-435-675B-4

Query Match 7.9%; Score 95; DB 1; Length 1873;
 Best Local Similarity 24.0%; Pred. No. 0.35;
 Matches 46; Conservative 31; Mismatches 31; Indels 69; Gaps 46; Gaps 9;

Qy 12 SNSCCLCCHVRTGTLGWLGYLLIAVVLILLSSA---DPDQYNNFSSSELGDFEPM 67

Query 112 SNSCCUCCHRTGTTLGGWWYLINAVVLLSALAA---DPOYNFSSSELGGDFEM 67
 Db 785 TNKVRVLCH---RIVNATW---TNPFLPLSSALAAEDPIRAESVRQIUYFD-- 836

Query 68 DDANMCIAAISLMLICAMATGYKQRAAWIIPPFQYQIFDPALMVLVAVTIVLYPN 127
 Db 837 ----IAFTSVTVEVLKMTTYGAFHKGS----PCTNYFNI-LDLVVAVSLL--- 881

Query 128 SIQEYIRQLPPNPYRDDVNSVNPTCLVLLFSTIILFKG--YLISCVWNYCYYRYING 185
 Db 882 ----SMGLESSTISVVKLRLVRPLRATNRAKGLKHHVQCVFVAIRTG 936

Db 882 ----SMGLESSTISVVKLRLVRPLRATNRAKGLKHHVQCVFVAIRTG 936

RESULT 11
 US-09-107-532A-4559
 Sequence 4559, Application US/09107532A
 ; Patent No. 658325

GENERAL INFORMATION:
 US-08-336-257A-7
 Sequence 7, Application US/08336257A
 ; Patent No. 5726035

APPLICANT: JAY, Scott D
 APPLICANT: Ellis, Steven B.
 APPLICANT: Harpold, Michael M.
 APPLICANT: Campbell, Kevin P.

ADDRESS: Brown, Martin, Haller & McClain
 STREET: 1660 Union Street
 CITY: San Diego
 STATE: CA
 COUNTRY: USA

ZIP: 92101-2926

COMPUTER READABLE FORM:
 COMPUTER TYPE: Discrete
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 1.5

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/336,257A
 FILING DATE: 07-NOV-1994
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: Seidman, Stephanie L.
 REGISTRATION NUMBER: 33,779
 REFERENCE/DOCKET NUMBER: 54898
 TELEPHONE: (619) 238-0999
 TELEFAX: (619) 238-0062

SEQUENCE CHARACTERISTICS:
 LENGTH: 1873 amino acids
 TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: Linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

ORIGINAL SOURCE:
 US-08-336-257A-7

Query Match 7.9%; Score 95; DB 1; Length 1873;
 Best Local Similarity 24.0%; Pred. No. 0.35; Mismatches 31; Indels 46; Gaps 9;

Matches 46; Conservative 31; Mismatches 69; Indels 46; Gaps 9;

Query 112 SNSCCUCCHRTGTTLGGWWYLINAVVLLSALAA---DPOYNFSSSELGGDFEM 67
 Db 785 TNKVRVLCH---RIVNATW---TNPFLPLSSALAAEDPIRAESVRQIUYFD-- 836

Query 68 DDANMCIAAISLMLICAMATGYKQRAAWIIPPFQYQIFDPALMVLVAVTIVLYPN 127
 Db 837 ----IAFTSVTVEVLKMTTYGAFHKGS----PCTNYFNI-LDLVVAVSLL--- 881

Qy 136 LPPNPYRDDVMSVPTCLVLIILFISIILTFKGYLISCV-----W - 177
 Db 298 SRP-----LKVN-LCTINICFLSMIL---LLISTKVNTHNRAENNNSLKVFR 343
 Qy 178 --NCYR----YINGRN-----SDPVLVVTTSNNTTFLPPYDADTVNGAAKE 218
 Db 344 TTNLXKTNITNQLNRMNTTVEENYLKCKSKFVKIQKNKTFIAPYNTATIQENNKE 401

RESULT 12

US 07-745-206A-2
 Sequence 2, Application US/07745206A
 Patent No. 5429921

GENERAL INFORMATION:

APPLICANT: Hartold, Michael
 APPLICANT: Ellis, Steven
 APPLICANT: McCue, Ann
 APPLICANT: Feldman, Daniel
 TITLE OF INVENTION: Human Calcium Channel Compositions and Methods
 NUMBER OF SEQUENCES: 32
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fitch, Evan, Tabin & Flannery
 STREET: 135 S. LaSalle
 CITY: Chicago
 STATE: Illinois
 COUNTRY: U.S.A.
 ZIP: 60603

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/745,206A
 FILING DATE: 19910815
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Feder, Scott B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-372-7842
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2161 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US--07-745-206A-2

Query Match 7.4%; Score 88.5; DB 1; Length 2161;
 Best Local Similarity 25.0%; Pred. No. 2; Matches 46; Conservative 34; Mismatches 61; Indels 43; Gaps 10;

Qy 21 VRTGTLGWLNAVLLSALA---DP-DQYNFSSSELG-GDPEFMDDANMCI 74
 Db 875 IRVGCKLKHIFHFLNLLFIMLSSAALAAEDPIRSHSRNTLGYFYAF----- 926
 Qy 75 AIAISLMLICAMATYGAJKQRAWIIPFFCYQIFDFALNMLVAITVLYPNSIQEYIR 134
 Db 927 -TAIFVTELL-KMFTFGFLHKGA---FCRNFNL-LDMLVVGVSLL----- 968
 Qy 135 QLPPNPYRDDVMSVPTCLVLIILFISIILTFLFGG--VLIJSCVNNCYRTINGRNNSDVL 192
 Db 969 ---SFGQSSAISVVKLRLVRLPRAINRAKGLKHVVQCVFAIRTI----GNIM 1019
 Qy 193 VVVT 196
 Db 1020 IVT 1023

US-08-455-543A-49
 Sequence 49, Application US/08455543A
 Patent No. 5798846

GENERAL INFORMATION:

APPLICANT: Harpold, Michael
 APPLICANT: Ellis, Steven
 APPLICANT: Williams, Mark
 APPLICANT: Feldman, Daniel
 APPLICANT: McCue, Ann
 APPLICANT: Brenner, Robert
 ADDRESSEE: Brown, Martin, Haller & McClain
 STREET: 1660 Union Street
 CITY: San Diego
 STATE: California
 COUNTRY: USA
 ZIP: 92101-2926
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/455,543A
 FILING DATE: May 31, 1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/223,305
 FILING DATE: April 4, 1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/868,354
 FILING DATE: April 10, 1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/745,206
 FILING DATE: 15-AUG-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/620,250
 FILING DATE: 30-NOV-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/482,384
 FILING DATE: 20-FEB-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/603,751
 FILING DATE: 04-APR-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US89/01408
 FILING DATE: 04-APR-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/176,899
 FILING DATE: 04-APR-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Seidman, Stephanie L.
 REGISTRATION NUMBER: 33,779
 REFERENCE/DOCKET NUMBER: 6362-52517
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619)238-0999
 TELEFAX: (619)238-0062
 INFORMATION FOR SEQ ID NO: 49:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2161 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 US-08-455-543A-49

Query Match 7.4%; Score 88.5; DB 1; Length 2161;
 Best Local Similarity 25.0%; Pred. No. 2; Matches 46; Conservative 34; Mismatches 61; Indels 43; Gaps 10;

Qy 21 VRTGTILLGVVYLITNAVVLILLSSALA----DP-DQYNPSSSEYLG-GDPEFMDDANMCI 74 ; REFERENCE/DOCKET NUMBER: 6362-52517 ;
 Db 875 IRVGCHKLHNPHLNLVPMSSALAAEDPTRSNSFNTILGYFDYAF----- 926 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 238-0999 ;
 Qy .75 AIAISLMLICAMATGGAYKORAAMIPPFYCQIDFDALMLVAITVLYPPNSIQEYIR 134 ; TELEFAX: (619) 238-0052 ;
 Db 927 -TAIPTVEILL-KMTTGFAPLHKGA---FCRNYFNL-LDMLVYGVSLV----- 968 ; INFORMATION FOR SEQ ID NO: 51 ;
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2161 amino acids
 ; TYPE: amino acid
 Qy 135 QLPNNPYRDMDMSVNPFTCLVLLPSTIILTFKG---YLISCVWNCYRYINGRNSSDVL 192 ; STRANDEDNESS: single
 ;
 Qy 969 ---SPOIQSSAISVVKLRLVRLRPLRAINRAKGLKHVVQCVFVAIRTI-----GNIM 1019 ; TOPOLOGY: linear
 Db 193 VVVT 196 ; MOLECULE TYPE: protein
 ; FRAGMENT TYPE: internal
 Qy 1020 IVTT 1023 ; US-08-455-543A-51

RESULT 14 ; Query Match 7.4%; Score 88.5%; DB 1; Length 2161;
 ; Best Local Similarity 25.0%; Pred. No. 2;
 ; Matches 46; Conservative 34; Mismatches 61; Indels 43; Gaps 10;

Qy 21 VRTGTILLGVVYLITNAVVLILLSSALA----DP-DQYNPSSSEYLG-GDPEFMDDANMCI 74 ;
 Db 875 IRVGCHKLHNPHLNLVPMSSALAAEDPTRSNSFNTILGYFDYAF----- 926 ;
 ;
 Qy 75 AIAISLMLICAMATGGAYKORAAMIPPFYCQIDFDALMLVAITVLYPPNSIQEYIR 134 ;
 Db 927 -TAIPTVEILL-KMTTGFAPLHKGA---FCRNYFNL-LDMLVYGVSLV----- 968 ;
 ;
 Qy 135 QLPNNPYRDMDMSVNPFTCLVLLPSTIILTFKG---YLISCVWNCYRYINGRNSSDVL 192 ;
 Db 969 ---SPOIQSSAISVVKLRLVRLRPLRAINRAKGLKHVVQCVFVAIRTI-----GNIM 1019 ;
 Qy 193 VVVT 196 ;
 Db 1020 IVTT 1023 ;

RESULT 15 ;
 US-08-223-305C-49 ;
 ; Sequence 49, Application US/08223305C ;
 ; Patent No. 5851B24 ;
 ; GENERAL INFORMATION:
 ; APPLICANT: Harpold, Michael
 ; APPLICANT: Ellis, Steven
 ; APPLICANT: Williams, Mark
 ; APPLICANT: Feldman, Daniel
 ; APPLICANT: McCue, Ann
 ; APPLICANT: Bremer, Robert
 ; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
 ; TITLE OF INVENTION: METHODS
 ; NUMBER OF SEQUENCES: 57
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Brown, Martin, Haller & McClain
 ; STREET: 1660 Union Street
 ; CITY: San Diego
 ; STATE: California
 ; ZIP: 92101-2926
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/455,543A
 ; FILING DATE: May 31, 1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/223,305
 ; FILING DATE: April 4, 1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/868,354
 ; FILING DATE: April 10, 1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/745,206
 ; FILING DATE: 15-AUG-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/620,250
 ; FILING DATE: 30-NOV-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/482,384
 ; FILING DATE: 20-FEB-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/603,751
 ; FILING DATE: 04-APR-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO PCT/US89/01408
 ; FILING DATE: 04-APR-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/176,899
 ; FILING DATE: 04-APR-1988
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Seidman, Stephanie L.
 ; REGISTRATION NUMBER: 33,779

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/482,384
 FILING DATE: 20-FEB-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/603,751
 FILING DATE: 04-APR-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US89/01408
 FILING DATE: 04-APR-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/176,899
 FILING DATE: 04-APR-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Seidman, Stephanie L.
 REGISTRATION NUMBER: 33,779
 REFERENCE/DOCKET NUMBER: 52516 (P519739)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 238-0999
 TELEFAX: (619) 238-0062
 INFORMATION FOR SEQ ID NO: 49:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2161 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 US-08-223-305C-49

Query Match 7.4%; Score 88.5; DB 2; Length 2161;
 Best Local Similarity 25.0%; Pred. No. 2;
 Matches 46; Conservative 34; Mismatches 61; Indels 43; Gaps 10;
 Query 21 VRTGTLILGWYLINAVVLLILSALA---DP-DQYNSSSEIG-GFEEFDNDANCI 74
 Database 875 IRVGCHKLINHIFTNLIVLIVFIMLSAAALAEDPIRSHFRNTLGYFYIAP----- 926
 Query 75 AIAISLMLMICAMATYGAVKQRARAWIIPPFYCQIFDFALANMLVAITLIVPNSIQEYTR 134
 Database 927 -TAIPTVEILL-KMFTFGAFLHKGAI---FCRNYFNL-LDMLVVGVSILV----- 966
 Query 135 QLPPNFPYRDDVMNSYNPTCLVILIFISIILTFPKG--YLISCVWNCTRYINGRNSSDVL 192
 Database 969 ---SFGIQSSAISVVKIRLVLVRPLRAINRAKGLKRVQCVCVFAIRTI----GNIM 1019
 Query 193 VYVT 196
 Database 1020 IVTT 1023

Search completed: February 2, 2004, 14:24:17
 Job time : 24 SECs

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OM protein - protein search, using sw model

Run on: February 2, 2004, 14:21:56 ; Search time 177 Seconds (without alignments)

Perfect score: 1200

Sequence: 1 MKMVAPTRFYSNSCCLCH YDDATVNGAAKEPQQPVSA 226

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 5728757 seqs, 909918778 residues

Total number of hits satisfying chosen parameters: 5728757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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28 892.5 74.4 301 1 PCT-US01-08656-1669

29 892.5 74.4 301 1 PCT-US02-07431-99

30 769 64.1 162 26 US-10-077-340-175

31 769 64.1 162 26 US-10-177-488-124

32 769 64.1 162 26 US-10-301-822-99

33 769 64.1 162 26 US-10-416-993-364

34 769 64.1 162 26 US-10-058-993-03

35 714 59.5 137 23 US-10-273-573-6669

36 714 59.5 137 23 US-09-852-659-03

37 714 59.5 137 23 US-09-852-659A-63

38 714 59.5 137 23 US-09-852-797-63

39 714 59.5 137 23 US-09-853-161-97

40 682 56.8 157 20 US-09-673-840A-244

41 553.5 46.1 221 20 US-09-641-377-413

42 553.5 46.1 233 1 PCT-US01-16450A-2149

43 553.5 46.1 233 1 PCT-US01-16450A-2149

44 553.5 46.1 233 28 US-10-264-237-2149

45 553.5 46.1 233 29 US-10-376-564-12

ALIGNMENTS

RESULT 1 PCT-US01-16450-1994

Sequence 1994, Application PC/TUS0116450

GENERAL INFORMATION:

APPLICANT: Human Genome Sciences, Inc.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA11PCT

CURRENT APPLICATION NUMBER: PC/TUS01/16450

CURRENT FILING DATE: 2001-06-01

PRIOR APPLICATION NUMBER: 60/205, 515

PRIOR FILING DATE: 2000-05-19

NUMBER OF SEQ ID NOS: 2830

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 1994

LENGTH: 226

TYPE: PRT

ORGANISM: Homo sapiens

PCT-US01-16450-1994

SUMMARIES

Query Match Score 100.0% ; Pred. No. 4 ; Seq-111; Description

Result No. Score Match Length DB ID Number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 1994, Ap

Query Match Score 100.0% ; Pred. No. 4 ; Seq-111; Description

Result No. Score Match Length DB ID Number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 1994, Ap

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RESULT 2
PCT-US01-16450A-1994
; Sequence 1994, Application PCT-US01-16450A
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; CURRENT APPLICATION NUMBER: PCT/US01/16450A
; CURRENT FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: 60/205, 515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2820
; SEQ ID NOS: 1994
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
; PCT-US01-16450A-1994

Query Match 100.0% Score 1200; DB 1; Length 226;
Best Local Similarity 100.0%; Pred. No. 4.8e-11;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKMVAAPTRFYSNSCCCLCHYRTGTLGWWYLINAVVLLILSALADPQYNFSSSL 60
1 GGDFFEMD DANNCIAIAISLMLICAMATGAYKORAANIPFFCYQIFDFALNLVAI 120
1 GGDFFEMD DANNCIAIAISLMLICAMATGAYKORAANIPFFCYQIFDFALNLVAI 120
121 TVLIYPNSI QEYIROLPPNPFPYRDDWSVNPTCLVLLIISIITLFGYLISCVWNCY 180
121 TVLIYPNSI QEYIROLPPNPFPYRDDWSVNPTCLVLLIISIITLFGYLISCVWNCY 180
181 RYINGRNSDVLVYVTSNDTTLPPYDATINGAAKEPPPYVSA 226
181 RYINGRNSDVLVYVTSNDTTLPPYDATINGAAKEPPPYVSA 226

RESULT 2
PCT-US01-16450A-1994
; Sequence 1994, Application PCT-US01-16450A
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; CURRENT APPLICATION NUMBER: PCT/US01/16450A
; CURRENT FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: 60/205, 515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2820
; SEQ ID NOS: 1994
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
; PCT-US01-16450A-1994

Query Match 100.0% Score 1200; DB 1; Length 226;
Best Local Similarity 100.0%; Pred. No. 4.8e-11;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKMVAAPTRFYSNSCCCLCHYRTGTLGWWYLINAVVLLILSALADPQYNFSSSL 60
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1 GGDFFEMD DANNCIAIAISLMLICAMATGAYKORAANIPFFCYQIFDFALNLVAI 120
121 TVLIYPNSI QEYIROLPPNPFPYRDDWSVNPTCLVLLIISIITLFGYLISCVWNCY 180
121 TVLIYPNSI QEYIROLPPNPFPYRDDWSVNPTCLVLLIISIITLFGYLISCVWNCY 180
181 RYINGRNSDVLVYVTSNDTTLPPYDATINGAAKEPPPYVSA 226
181 RYINGRNSDVLVYVTSNDTTLPPYDATINGAAKEPPPYVSA 226

RESULT 4
US-09-611-523-2
; Sequence 2, Application US/09611523
; GENERAL INFORMATION:
; APPLICANT: OTA, TOSHI
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: NISHIKAWA, TETSUO
; APPLICANT: KAWAI, YURI
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: HAYASHI, KOJI
; TITLE OF INVENTION: SECRETORY PROTEIN OR MEMBRANE PROTEIN
; FILE REFERENCE: 08435/0121
; CURRENT APPLICATION NUMBER: US/09/611, 523
; CURRENT FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: JP 1999-194179
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: JP 2000-118775
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183766
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 60/159, 586
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 60/183, 323
; PRIOR FILING DATE: 2000-02-17
; NUMBER OF SEQ ID NOS: 679
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-611-523-2

Query Match 100.0% Score 1200; DB 20; Length 226;
Best Local Similarity 100.0%; Pred. No. 4.8e-11;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
US-09-488-725A-2720
; Sequence 2720, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc.
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488, 725A
; PRIOR APPLICATION NUMBER: US/09/488, 725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US/09/552, 317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US/09/598, 042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US/09/620, 312
; PRIOR FILING DATE: 2000-11-22
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488, 725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 714
; SOFTWARE: bc_fpl_Genes_b Versions 1.0
; SEQ ID NO 2
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-488-725A-2720

Qy 1 MKMVAAPWTRPYSNSCCCLCHYRTGTLILLISALADPQYNPSSSL 60
 Db 1 MKMVAAPWTRPYSNSCCCLCHYRTGTLILLISALADPQYNPSSSL 60

Qy 61 GGDPEPMDDANMCIAAISLIMICAMATGAYKORAAWLTIPFCYQIFDFALNLVAI 120
 Db 61 GGDPEPMDDANMCIAAISLIMICAMATGAYKORAAWLTIPFCYQIFDFALNLVAI 120

Qy 121 TVLIYPNSIQEYIROLPPNPYRDDMSVNPCTCLVLIILFISIILTFKGYLISCVWNCY 180
 Db 121 TVLIYPNSIQEYIROLPPNPYRDDMSVNPCTCLVLIILFISIILTFKGYLISCVWNCY 180

Qy 161 RYINGRNSDVLVYVTSNDTIVLPPYDDATNGAAKEPPPYVSA 226
 Db 161 RYINGRNSDVLVYVTSNDTIVLPPYDDATNGAAKEPPPYVSA 226

Qy 181 RYINGRNSDVLVYVTSNDTIVLPPYDDATNGAAKEPPPYVSA 226
 Db 181 RYINGRNSDVLVYVTSNDTIVLPPYDDATNGAAKEPPPYVSA 226

RESULT 5
 US-09-641-377-412
 ; Sequence 412, Application US/09641377
 ; GENERAL INFORMATION:
 ; APPLICANT: WIEMANN, STEFAN
 ; APPLICANT: GASSENHUBER, JOHANN
 ; TITLE OF INVENTION: HUMAN DNA SEQUENCES
 ; FILE REFERENCE: 08/1100/0106
 ; CURRENT APPLICATION NUMBER: US/09/641,377
 ; CURRENT FILING DATE: 2000-08-18
 ; PRIOR APPLICATION NUMBER: 60/149,499
 ; PRIOR FILING DATE: 1999-08-18
 ; PRIOR APPLICATION NUMBER: 60/156,503
 ; PRIOR FILING DATE: 1999-09-28
 ; NUMBER OF SEQ ID NOS: 1793
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO: 412
 ; LENGTH: 226
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-641-377-412

Query Match 100.0%; Score 1200; DB 20; Length 226;
 Best Local Similarity 100.0%; Pred. No. 4.8e-111;
 Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKMVAAPWTRPYSNSCCCLCHYRTGTLILLISALADPQYNPSSSL 60
 Db 1 MKMVAAPWTRPYSNSCCCLCHYRTGTLILLISALADPQYNPSSSL 60

Qy 61 GGDPEPMDDANMCIAAISLIMICAMATGAYKORAAWLTIPFCYQIFDFALNLVAI 120
 Db 61 GGDPEPMDDANMCIAAISLIMICAMATGAYKORAAWLTIPFCYQIFDFALNLVAI 120

Qy 121 TVLIYPNSIQEYIROLPPNPYRDDMSVNPCTCLVLIILFISIILTFKGYLISCVWNCY 180
 Db 121 TVLIYPNSIQEYIROLPPNPYRDDMSVNPCTCLVLIILFISIILTFKGYLISCVWNCY 180

Qy 161 RYINGRNSDVLVYVTSNDTIVLPPYDDATNGAAKEPPPYVSA 226
 Db 161 RYINGRNSDVLVYVTSNDTIVLPPYDDATNGAAKEPPPYVSA 226

Qy 181 RYINGRNSDVLVYVTSNDTIVLPPYDDATNGAAKEPPPYVSA 226
 Db 181 RYINGRNSDVLVYVTSNDTIVLPPYDDATNGAAKEPPPYVSA 226

RESULT 6
 US-09-743-247A-92
 ; Sequence 92, Application US/09743247A
 ; GENERAL INFORMATION:
 ; APPLICANT: Sagami Chemical Research Center; Proteogene Inc.
 ; TITLE OF INVENTION: Human Proteins Having Hydrophobic Domains And DNAs Encoding These
 ; FILE REFERENCE: 1997-13300
 ; CURRENT APPLICATION NUMBER: US/09/743,247A
 ; CURRENT FILING DATE: 1999-07-22
 ; PRIOR APPLICATION NUMBER: JP 10-208820
 ; PRIOR FILING DATE: 1998-07-22

Query Match 100.0%; Score 1200; DB 25; Length 226;
 Best Local Similarity 100.0%; Pred. No. 4.8e-111;
 Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKMVAAPWTRPYSNSCCCLCHYRTGTLILLISALADPQYNPSSSL 60
 Db 1 MKMVAAPWTRPYSNSCCCLCHYRTGTLILLISALADPQYNPSSSL 60

Qy 61 GGDPEPMDDANMCIAAISLIMICAMATGAYKORAAWLTIPFCYQIFDFALNLVAI 120
 Db 61 GGDPEPMDDANMCIAAISLIMICAMATGAYKORAAWLTIPFCYQIFDFALNLVAI 120

Qy 121 TVLIYPNSIQEYIROLPPNPYRDDMSVNPCTCLVLIILFISIILTFKGYLISCVWNCY 180
 Db 121 TVLIYPNSIQEYIROLPPNPYRDDMSVNPCTCLVLIILFISIILTFKGYLISCVWNCY 180

Qy 161 RYINGRNSDVLVYVTSNDTIVLPPYDDATNGAAKEPPPYVSA 226
 Db 161 RYINGRNSDVLVYVTSNDTIVLPPYDDATNGAAKEPPPYVSA 226

RESULT 5
 US-09-641-377-412
 ; Sequence 412, Application US/09641377
 ; GENERAL INFORMATION:
 ; APPLICANT: WIEMANN, STEFAN
 ; APPLICANT: GASSENHUBER, JOHANN
 ; TITLE OF INVENTION: HUMAN DNA SEQUENCES
 ; FILE REFERENCE: 08/1100/0106
 ; CURRENT APPLICATION NUMBER: US/09/641,377
 ; CURRENT FILING DATE: 2000-08-18
 ; PRIOR APPLICATION NUMBER: 60/149,499
 ; PRIOR FILING DATE: 1999-08-18
 ; PRIOR APPLICATION NUMBER: 60/156,503
 ; PRIOR FILING DATE: 1999-09-28
 ; NUMBER OF SEQ ID NOS: 1793
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO: 412
 ; LENGTH: 226
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-641-377-412

Query Match 100.0%; Score 1200; DB 21; Length 226;
 Best Local Similarity 100.0%; Pred. No. 4.8e-111;
 Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKMVAAPWTRPYSNSCCCLCHYRTGTLILLISALADPQYNPSSSL 60
 Db 1 MKMVAAPWTRPYSNSCCCLCHYRTGTLILLISALADPQYNPSSSL 60

Qy 61 GGDPEPMDDANMCIAAISLIMICAMATGAYKORAAWLTIPFCYQIFDFALNLVAI 120
 Db 61 GGDPEPMDDANMCIAAISLIMICAMATGAYKORAAWLTIPFCYQIFDFALNLVAI 120

Qy 121 TVLIYPNSIQEYIROLPPNPYRDDMSVNPCTCLVLIILFISIILTFKGYLISCVWNCY 180
 Db 121 TVLIYPNSIQEYIROLPPNPYRDDMSVNPCTCLVLIILFISIILTFKGYLISCVWNCY 180

Qy 161 RYINGRNSDVLVYVTSNDTIVLPPYDDATNGAAKEPPPYVSA 226
 Db 161 RYINGRNSDVLVYVTSNDTIVLPPYDDATNGAAKEPPPYVSA 226

Qy 121 TVLIYPNSIQEYIROLPPNPYRDDMSVNPCTCLVLIILFISIILTFKGYLISCVWNCY 180
 Db 121 TVLIYPNSIQEYIROLPPNPYRDDMSVNPCTCLVLIILFISIILTFKGYLISCVWNCY 180

Qy 161 RYINGRNSDVLVYVTSNDTIVLPPYDDATNGAAKEPPPYVSA 226
 Db 161 RYINGRNSDVLVYVTSNDTIVLPPYDDATNGAAKEPPPYVSA 226

Qy 121 TVLIYPNSIQEYIROLPPNPYRDDMSVNPCTCLVLIILFISIILTFKGYLISCVWNCY 180
 Db 121 TVLIYPNSIQEYIROLPPNPYRDDMSVNPCTCLVLIILFISIILTFKGYLISCVWNCY 180

Qy 161 RYINGRNSDVLVYVTSNDTIVLPPYDDATNGAAKEPPPYVSA 226
 Db 161 RYINGRNSDVLVYVTSNDTIVLPPYDDATNGAAKEPPPYVSA 226

Qy 121 TVLIYPNSIQEYIROLPPNPYRDDMSVNPCTCLVLIILFISIILTFKGYLISCVWNCY 180
 Db 121 TVLIYPNSIQEYIROLPPNPYRDDMSVNPCTCLVLIILFISIILTFKGYLISCVWNCY 180

Qy 161 RYINGRNSDVLVYVTSNDTIVLPPYDDATNGAAKEPPPYVSA 226
 Db 161 RYINGRNSDVLVYVTSNDTIVLPPYDDATNGAAKEPPPYVSA 226

Qy 121 TVLIYPNSIQEYIROLPPNPYRDDMSVNPCTCLVLIILFISIILTFKGYLISCVWNCY 180
 Db 121 TVLIYPNSIQEYIROLPPNPYRDDMSVNPCTCLVLIILFISIILTFKGYLISCVWNCY 180

Qy 161 RYINGRNSDVLVYVTSNDTIVLPPYDDATNGAAKEPPPYVSA 226
 Db 161 RYINGRNSDVLVYVTSNDTIVLPPYDDATNGAAKEPPPYVSA 226

Qy 121 TVLIYPNSIQEYIROLPPNPYRDDMSVNPCTCLVLIILFISIILTFKGYLISCVWNCY 180
 Db 121 TVLIYPNSIQEYIROLPPNPYRDDMSVNPCTCLVLIILFISIILTFKGYLISCVWNCY 180

Qy 161 RYINGRNSDVLVYVTSNDTIVLPPYDDATNGAAKEPPPYVSA 226
 Db 161 RYINGRNSDVLVYVTSNDTIVLPPYDDATNGAAKEPPPYVSA 226

Qy 121 TVLIYPNSIQEYIROLPPNPYRDDMSVNPCTCLVLIILFISIILTFKGYLISCVWNCY 180
 Db 121 TVLIYPNSIQEYIROLPPNPYRDDMSVNPCTCLVLIILFISIILTFKGYLISCVWNCY 180

Qy 161 RYINGRNSDVLVYVTSNDTIVLPPYDDATNGAAKEPPPYVSA 226
 Db 161 RYINGRNSDVLVYVTSNDTIVLPPYDDATNGAAKEPPPYVSA 226

Qy 121 TVLIYPNSIQEYIROLPPNPYRDDMSVNPCTCLVLIILFISIILTFKGYLISCVWNCY 180
 Db 121 TVLIYPNSIQEYIROLPPNPYRDDMSVNPCTCLVLIILFISIILTFKGYLISCVWNCY 180

Qy 161 RYINGRNSDVLVYVTSNDTIVLPPYDDATNGAAKEPPPYVSA 226
 Db 161 RYINGRNSDVLVYVTSNDTIVLPPYDDATNGAAKEPPPYVSA 226

Db 1 MKMVAAPWTRFYSNSCCLCCHVRGTILLGWLILNAVVLILSALADDQYNFSSSEL 60
 Qy 61 GGDFFEMDAMCIAAISLIMILICAMATGAYKORAAWIPPFCCYQLEDFALNLVIAI 120
 Db 61 GGDFFEMDAMCIAAISLIMILICAMATGAYKORAAWIPPFCCYQLEDFALNLVIAI 120
 Qy 121 TVLIYPNSIQEYIROLPPNPYRDDMSNPTCLVLILFISILTFKGYLISCVNRY 180
 Db 121 TVLIYPNSIQEYIROLPPNPYRDDMSNPTCLVLILFISILTFKGYLISCVNRY 180
 Qy 181 RYINGRNSSDLVVYTTSNDTIVLPPYDATVNGAAKEPPPPVYSA 226
 Db 181 RYINGRNSSDLVVYTTSNDTIVLPPYDATVNGAAKEPPPPVYSA 226
 Qy 181 RYINGRNSSDLVVYTTSNDTIVLPPYDATVNGAAKEPPPPVYSA 226

RESULT 8

US-09-969-680A-26

/ Sequence 26, Application US/09969680A

/ GENERAL INFORMATION:

/ APPLICANT: LAL, Preeti; YUE, Henry

/ APPLICANT: TANG, Y. Tom

/ APPLICANT: BANDMAN, Olga

/ APPLICANT: BURFORD, Neil

/ APPLICANT: AZIMZAI, Yalda

/ APPLICANT: BAUGHN, Mariah R.

/ APPLICANT: LU, Dzung Aina M.

/ APPLICANT: PATTISON, Chandra

/ TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS

/ CURRENT APPLICATION NUMBER: US/09/969,680A

/ CURRENT FILING DATE: 2001-10-02

/ PRIOR APPLICATION NUMBER: US/0/22315

/ PRIOR FILING DATE: 2000-08-14

/ PRIOR APPLICATION NUMBER: 60/149,641

/ PRIOR FILING DATE: 1999-08-17

/ PRIOR APPLICATION NUMBER: 60/164,203

/ PRIOR FILING DATE: 1999-11-09

/ NUMBER OF SEQ ID NOS: 74

/ SOFTWARE: PERL Program

/ SEQ ID NO: 26

/ LENGTH: 226

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ FEATURE: NAME/KEY: misc_feature

/ OTHER INFORMATION: Incyte ID No: 2795577CD1

/ SEQ ID NO: 26

/ LENGTH: 226

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ FEATURE: NAME/KEY: misc_feature

/ OTHER INFORMATION: Incyte ID No: 2795577CD1

/ SEQ ID NO: 26

/ LENGTH: 226

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ FEATURE: NAME/KEY: misc_feature

/ OTHER INFORMATION: Incyte ID No: 2795577CD1

/ SEQ ID NO: 26

/ LENGTH: 226

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ FEATURE: NAME/KEY: misc_feature

/ OTHER INFORMATION: Incyte ID No: 2795577CD1

/ SEQ ID NO: 26

/ LENGTH: 226

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ FEATURE: NAME/KEY: misc_feature

/ OTHER INFORMATION: Incyte ID No: 2795577CD1

/ SEQ ID NO: 26

/ LENGTH: 226

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ FEATURE: NAME/KEY: misc_feature

/ OTHER INFORMATION: Incyte ID No: 2795577CD1

/ SEQ ID NO: 26

/ LENGTH: 226

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ FEATURE: NAME/KEY: misc_feature

/ OTHER INFORMATION: Incyte ID No: 2795577CD1

/ SEQ ID NO: 26

/ LENGTH: 226

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ FEATURE: NAME/KEY: misc_feature

/ OTHER INFORMATION: Incyte ID No: 2795577CD1

/ SEQ ID NO: 26

/ LENGTH: 226

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ FEATURE: NAME/KEY: misc_feature

/ OTHER INFORMATION: Incyte ID No: 2795577CD1

/ SEQ ID NO: 26

/ LENGTH: 226

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ FEATURE: NAME/KEY: misc_feature

/ OTHER INFORMATION: Incyte ID No: 2795577CD1

/ SEQ ID NO: 26

/ LENGTH: 226

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ FEATURE: NAME/KEY: misc_feature

/ OTHER INFORMATION: Incyte ID No: 2795577CD1

/ SEQ ID NO: 26

/ LENGTH: 226

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ FEATURE: NAME/KEY: misc_feature

/ OTHER INFORMATION: Incyte ID No: 2795577CD1

/ SEQ ID NO: 26

/ LENGTH: 226

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ FEATURE: NAME/KEY: misc_feature

/ OTHER INFORMATION: Incyte ID No: 2795577CD1

/ SEQ ID NO: 26

/ LENGTH: 226

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ FEATURE: NAME/KEY: misc_feature

/ OTHER INFORMATION: Incyte ID No: 2795577CD1

/ SEQ ID NO: 26

/ LENGTH: 226

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ FEATURE: NAME/KEY: misc_feature

/ OTHER INFORMATION: Incyte ID No: 2795577CD1

/ SEQ ID NO: 26

/ LENGTH: 226

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ FEATURE: NAME/KEY: misc_feature

/ OTHER INFORMATION: Incyte ID No: 2795577CD1

/ SEQ ID NO: 26

/ LENGTH: 226

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ FEATURE: NAME/KEY: misc_feature

/ OTHER INFORMATION: Incyte ID No: 2795577CD1

/ SEQ ID NO: 26

/ LENGTH: 226

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ FEATURE: NAME/KEY: misc_feature

/ OTHER INFORMATION: Incyte ID No: 2795577CD1

/ SEQ ID NO: 26

/ LENGTH: 226

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ FEATURE: NAME/KEY: misc_feature

/ OTHER INFORMATION: Incyte ID No: 2795577CD1

/ SEQ ID NO: 26

/ LENGTH: 226

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ FEATURE: NAME/KEY: misc_feature

/ OTHER INFORMATION: Incyte ID No: 2795577CD1

/ SEQ ID NO: 26

/ LENGTH: 226

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ FEATURE: NAME/KEY: misc_feature

/ OTHER INFORMATION: Incyte ID No: 2795577CD1

/ SEQ ID NO: 26

/ LENGTH: 226

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ FEATURE: NAME/KEY: misc_feature

/ OTHER INFORMATION: Incyte ID No: 2795577CD1

/ SEQ ID NO: 26

/ LENGTH: 226

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ FEATURE: NAME/KEY: misc_feature

/ OTHER INFORMATION: Incyte ID No: 2795577CD1

/ SEQ ID NO: 26

/ LENGTH: 226

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ FEATURE: NAME/KEY: misc_feature

/ OTHER INFORMATION: Incyte ID No: 2795577CD1

/ SEQ ID NO: 26

/ LENGTH: 226

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ FEATURE: NAME/KEY: misc_feature

/ OTHER INFORMATION: Incyte ID No: 2795577CD1

/ SEQ ID NO: 26

/ LENGTH: 226

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ FEATURE: NAME/KEY: misc_feature

/ OTHER INFORMATION: Incyte ID No: 2795577CD1

/ SEQ ID NO: 26

/ LENGTH: 226

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ FEATURE: NAME/KEY: misc_feature

/ OTHER INFORMATION: Incyte ID No: 2795577CD1

/ SEQ ID NO: 26

/ LENGTH: 226

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ FEATURE: NAME/KEY: misc_feature

/ OTHER INFORMATION: Incyte ID No: 2795577CD1

/ SEQ ID NO: 26

/ LENGTH: 226

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ FEATURE: NAME/KEY: misc_feature

/ OTHER INFORMATION: Incyte ID No: 2795577CD1

/ SEQ ID NO: 26

/ LENGTH: 226

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ FEATURE: NAME/KEY: misc_feature

/ OTHER INFORMATION: Incyte ID No: 2795577CD1

/ SEQ ID NO: 26

/ LENGTH: 226

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ FEATURE: NAME/KEY: misc_feature

/ OTHER INFORMATION: Incyte ID No: 2795577CD1

/ SEQ ID NO: 26

/ LENGTH: 226

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ FEATURE: NAME/KEY: misc_feature

/ OTHER INFORMATION: Incyte ID No: 2795577CD1

/ SEQ ID NO: 26

/ LENGTH: 226

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ FEATURE: NAME/KEY: misc_feature

/ OTHER INFORMATION: Incyte ID No: 2795577CD1

/ SEQ ID NO: 26

/ LENGTH: 226

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ FEATURE: NAME/KEY: misc_feature

/ OTHER INFORMATION: Incyte ID No: 2795577CD1

/ SEQ ID NO: 26

/ LENGTH: 226

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ FEATURE: NAME/KEY: misc_feature

/ OTHER INFORMATION: Incyte ID No: 2795577CD1

/ SEQ ID NO: 26

/ LENGTH: 226

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ FEATURE: NAME/KEY: misc_feature

/ OTHER INFORMATION: Incyte ID No: 2795577CD1

/ SEQ ID NO: 26

/ LENGTH: 226

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ FEATURE: NAME/KEY: misc_feature

/ OTHER INFORMATION: Incyte ID No: 2795577CD1

/ SEQ ID NO: 26

/ LENGTH: 226

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ FEATURE: NAME/KEY: misc_feature

/ OTHER INFORMATION: Incyte ID No: 2795577CD1

/ SEQ ID NO: 26

/ LENGTH: 226

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ FEATURE: NAME/KEY: misc_feature

/ OTHER INFORMATION: Incyte ID No: 2795577CD1

/ SEQ ID NO: 26

/ LENGTH: 226

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ FEATURE: NAME/KEY: misc_feature

/ OTHER INFORMATION: Incyte ID No: 2795577CD1

/ SEQ ID NO: 26

/ LENGTH: 226

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ FEATURE: NAME/KEY: misc_feature

/ OTHER INFORMATION: Incyte ID No: 2795577CD1

/ SEQ ID NO: 26

/ LENGTH: 226

NUMBER OF SEQ ID NOS: 7143
 SOFTWARE: pc_Fl_Genes_b Versions 1.0
 SEQ ID NO: 2720
 LENGTH: 226
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-286-897-2720

Query Match 100.0%; Score 1200; DB 28; Length 226;
 Best Local Similarity 100.0%; Pred. No. 4 8e-111;
 Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 15
 US-09-488-725A-6292
 Sequence 6292, Application US/09488725A
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq, Inc
 ; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
 ; FILE REFERENCE: 784FLPCT
 ; CURRENT APPLICATION NUMBER: US/09/488,725A
 ; CURRENT FILING DATE: 2000-12-22
 ; PRIORITY APPLICATION NUMBER: US/09/488,725
 ; PRIORITY FILING DATE: 2000-01-21
 ; PRIORITY APPLICATION NUMBER: US09/552,317
 ; PRIORITY FILING DATE: 2000-04-25
 ; PRIORITY APPLICATION NUMBER: US09/598,042
 ; PRIORITY FILING DATE: 2000-06-20
 ; PRIORITY APPLICATION NUMBER: US09/620,312
 ; PRIORITY FILING DATE: 2000-07-19
 ; PRIORITY APPLICATION NUMBER: US09/653,450
 ; PRIORITY FILING DATE: 2000-08-31
 ; PRIORITY APPLICATION NUMBER: US09/662,191
 ; PRIORITY FILING DATE: 2000-09-14
 ; PRIORITY APPLICATION NUMBER: US09/693,036
 ; PRIORITY FILING DATE: 2000-10-19
 ; PRIORITY APPLICATION NUMBER: US09/727,344
 ; PRIORITY FILING DATE: 2000-11-29
 ; NUMBER OF SEQ ID NOS: 7144
 ; SOFTWARE: pc_Fl_Genes_b Versions 1.0
 ; SEQ ID NO: 6292
 ; LENGTH: 231
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-488-725A-6292

Query Match 100.0%; Score 1200; DB 18; Length 231;
 Best Local Similarity 100.0%; Pred. No. 4 9e-111;
 Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 14
 US-10-305-271B-2
 ; Sequence 2, Application US/10305278
 ; GENERAL INFORMATION:
 ; APPLICANT: OTA, TOSHI
 ; APPLICANT: ISOGAI, TAKAO
 ; APPLICANT: NISHIKAWA, TETSUO
 ; APPLICANT: KAWAI, YURI
 ; APPLICANT: SUGIYAMA, TOMOYASU
 ; APPLICANT: HAYASHI, KOJI
 ; TITLE OF INVENTION: SECRETORY PROTEIN OR MEMBRANE PROTEIN
 ; CURRENT APPLICATION NUMBER: US/10/305,278
 ; CURRENT FILING DATE: 2002-11-27
 ; PRIORITY APPLICATION NUMBER: US/09/611,523
 ; PRIORITY FILING DATE: 2000-07-07
 ; PRIORITY APPLICATION NUMBER: JP 1999-194179
 ; PRIORITY FILING DATE: 1999-07-08
 ; PRIORITY APPLICATION NUMBER: JP 2000-118775
 ; PRIORITY APPLICATION NUMBER: JP 2000-183765
 ; PRIORITY FILING DATE: 2000-05-02
 ; PRIORITY APPLICATION NUMBER: 60/159,586
 ; PRIORITY FILING DATE: 1999-10-18
 ; PRIORITY APPLICATION NUMBER: 60/183,323
 ; PRIORITY FILING DATE: 2000-02-17
 ; NUMBER OF SEQ ID NOS: 679
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 2
 ; LENGTH: 226
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-305-271B-2

Query Match 100.0%; Score 1200; DB 29; Length 226;
 Best Local Similarity 100.0%; Pred. No. 4 8e-111;
 Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 16
 US-09-488-725A-6292
 Sequence 6292, Application US/09488725A
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq, Inc
 ; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
 ; FILE REFERENCE: 784FLPCT
 ; CURRENT APPLICATION NUMBER: US/09/488,725A
 ; CURRENT FILING DATE: 2000-12-22
 ; PRIORITY APPLICATION NUMBER: US/09/488,725
 ; PRIORITY FILING DATE: 2000-01-21
 ; PRIORITY APPLICATION NUMBER: US09/552,317
 ; PRIORITY FILING DATE: 2000-04-25
 ; PRIORITY APPLICATION NUMBER: US09/598,042
 ; PRIORITY FILING DATE: 2000-06-20
 ; PRIORITY APPLICATION NUMBER: US09/620,312
 ; PRIORITY FILING DATE: 2000-07-19
 ; PRIORITY APPLICATION NUMBER: US09/653,450
 ; PRIORITY FILING DATE: 2000-08-31
 ; PRIORITY APPLICATION NUMBER: US09/662,191
 ; PRIORITY FILING DATE: 2000-09-14
 ; PRIORITY APPLICATION NUMBER: US09/693,036
 ; PRIORITY FILING DATE: 2000-10-19
 ; PRIORITY APPLICATION NUMBER: US09/727,344
 ; PRIORITY FILING DATE: 2000-11-29
 ; NUMBER OF SEQ ID NOS: 7144
 ; SOFTWARE: pc_Fl_Genes_b Versions 1.0
 ; SEQ ID NO: 6292
 ; LENGTH: 231
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-488-725A-6292

Query Match 100.0%; Score 1200; DB 29; Length 226;
 Best Local Similarity 100.0%; Pred. No. 4 8e-111;
 Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: February 2, 2004, 14:27:26
 Job time : 179 secs

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OM protein - protein search, using sw model

Run on: February 2, 2004, 14:22:31 ; Search time 24 Seconds
(without alignments)

724.790 Million cell updates/sec

Title: US-09-965-529-26

Perfect score: 1200

Sequence: 1 NKKMVAAPWTRFYSNSCCLCCH.....YDDATYNGAAKEKPPPYVSA 226

Scoring table: BLOSUM62

Gapext 0.5

Searched: 370304 seqs, 76968869 residues

Total number of hits satisfying chosen parameters: 370304

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA New:*

1: /cgn2_6/podata/1/paa/1/pct NEW COMB.pep:*

2: /cgn2_6/podata/1/paa/1/pct NEW COMB.pep:*

3: /cgn2_6/podata/1/paa/1/pct NEW COMB.pep:*

4: /cgn2_6/podata/1/paa/1/pct NEW COMB.pep:*

5: /cgn2_6/podata/1/paa/1/pct NEW COMB.pep:*

6: /cgn2_6/podata/1/paa/1/pct NEW COMB.pep:*

7: /cgn2_6/podata/1/paa/1/pct NEW COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	1200	100.0	283	6	US-10-734-564-97	Sequence 97, App1	Sequence 97, App1
2	1200	100.0	317	6	US-10-700-439-119	Sequence 119, App	Sequence 119, App
3	1181	98.4	234	1	PCT-US03-38808-248	Sequence 248, App	Sequence 248, App
4	1161	96.8	233	1	PCT-US03-38808-240	Sequence 240, App	Sequence 240, App
5	1144	95.3	319	1	PCT-US03-38808-241	Sequence 241, App	Sequence 241, App
6	282	23.5	425	5	US-09-614-150A-26129	Sequence 36129, App	Sequence 36129, App
7	282	23.5	432	5	US-09-614-150A-479	Sequence 447129, App	Sequence 447129, App
8	175	14.6	262	1	PCT-US02-41798A-33	Sequence 33, App1	Sequence 33, App1
9	153	12.8	205	1	PCT-US03-37278-7	Sequence 7, App1	Sequence 7, App1
10	122	10.2	165	5	US-09-614-150A-2447	Sequence 42447, App	Sequence 42447, App
11	101	8.4	260	6	US-10-415-182A-4106	Sequence 4106, App	Sequence 4106, App
12	97.5	8.1	1772	6	US-10-726-216-16	Sequence 16, App1	Sequence 16, App1
13	95	7.9	1873	5	US-10-726-216-22	Sequence 22, App1	Sequence 22, App1
14	94	7.8	250	5	US-09-614-150A-207	Sequence 207, App	Sequence 207, App
15	91	7.6	551	6	US-10-679-063-24094	Sequence 24094, App	Sequence 24094, App
16	89	7.4	241	5	US-09-614-150A-30138	Sequence 30138, App	Sequence 30138, App
17	89	7.4	1633	1	PCT-US03-30720-722	Sequence 722, App	Sequence 722, App
18	88.5	7.4	1755	6	US-10-322-696A-51	Sequence 51, App1	Sequence 51, App1
19	88.5	7.4	1755	6	US-10-322-696B-51	Sequence 51, App1	Sequence 51, App1
20	88.5	7.4	2166	6	US-10-726-216-4	Sequence 4, App1	Sequence 4, App1
21	88.5	7.4	2181	5	US-09-978-958-284	Sequence 288, App1	Sequence 288, App1
22	88.5	7.4	2181	6	US-10-322-696A-54	Sequence 54, App1	Sequence 54, App1
23	88.5	7.4	2181	6	US-10-726-216-18	Sequence 18, App1	Sequence 18, App1
24	88.5	7.4	2181	6	US-10-726-216-20	Sequence 20, App1	Sequence 20, App1
25	88.5	7.4	2181	6	US-10-322-696B-54	Sequence 54, App1	Sequence 54, App1
26	88	7.3	537	6	US-10-679-063-23292	Sequence 23292, App	Sequence 23292, App

ALIGMENTS

RESULT 1
US-10-734-564-97
Sequence 97, Application US/10734564

; GENERAL INFORMATION:
; APPLICANT: Christopher C Burgess et al
; TITLE OF INVENTION: Detection Methods Using TRIMP1
; FILE REFERENCE: 1657/2012
; CURRENT APPLICATION NUMBER: US/10/734,564
; CURRENT FILING DATE: 2003-12-12
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-734-564-97

Query Match 100.0%; Score 1200; DB 6; Length 283;
Best Local Similarity 100.0%; Pred. No. 2, 1e-114;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
US-10-700-439-119
Sequence 119, Application US/10700439
; GENERAL INFORMATION:
; APPLICANT: Mayo Foundation for Medical Education and Research
; APPLICANT: Bayer Healthcare LLC
; APPLICANT: Murex, Christopher
; APPLICANT: Myerow, Susan
; APPLICANT: Thigalingam, Arunthathai
; APPLICANT: Maini, Peter
; APPLICANT: Molino, Gary

APPLICANT: Burgart, Lawrence
 APPLICANT: Boardman, Lisa A.
 APPLICANT: Thibodeau, Steven
 APPLICANT: Lewis, Marcia
 APPLICANT: Lewis, Marcia
 TITLE OF INVENTION: Use of Differentially Expressed Nucleic Acid Sequences as
 FILE REFERENCE: 1657/2022
 CURRENT APPLICATION NUMBER: US/10/700,439
 NUMBER OF SEQ ID NOS: 186
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 119
 LENGTH: 317
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-700-439-119

Query Match 100.0%; Score 1200; DB 6; Length 317;
 Best Local Similarity 100.0%; Pred. No. 2.4e-114;
 Matches 226; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 MKMVA[PWTRFYSNSCLCCHVRTGTLGWLILNAVVLILSALADPQYNESSL 60
 Db 92 MKMVA[PWTRFYSNSCLCCHVRTGTLGWLILNAVVLILSALADPQYNESSL 151

Qy 61 GGDFFEMDDANMCIAIAISLMLICAMATYGA[KORAM]IIPFFCYQIFDFALNMLVAI 120
 Db 152 GGDFFEMDDANMCIAIAISLMLICAMATYGA[KORAM]IIPFFCYQIFDFALNMLVAI 211

Qy 121 TVLYPNSI[QEY]TROLPPNPFYRDDMSNPTCLVLILFISITLTFKGYLISCVNNCY 180
 Db 212 TVLYPNSI[QEY]TROLPPNPFYRDDMSNPTCLVLILFISITLTFKGYLISCVNNCY 271

Qy 181 RYINGRNSDVLVYTTSNDT[VL]LPYDDATVNGA[KE]PPPPYSA 226
 Db 272 RYINGRNSDVLVYTTSNDT[VL]LPYDDATVNGA[KE]PPPPYSA 317

RESULT 3
 PCT-US03-38808-248
 / Sequence 248, Application PC/TUS0338808
 / GENERAL INFORMATION:
 / APPLICANT: diadexus, Inc.
 / APPLICANT: Macina, Roberto
 / APPLICANT: Turner, Leah
 / APPLICANT: Sun, Yongming
 / APPLICANT: Rodriguez, Maria
 / APPLICANT: Tim Burcham
 / TITLE OF INVENTION: Compositions, Splice Variants and Methods Relating to Colon Speci
 / CURRENT APPLICATION NUMBER: PCT/US03/38808
 / CURRENT FILING DATE: 2003-12-04
 / PRIOR APPLICATION NUMBER: US 60/431,133
 / PRIOR FILING DATE: 2002-12-04
 / NUMBER OF SEQ ID NOS: 254
 / SOFTWARE: PatentIn version 3.1
 / SEQ ID NO: 254
 / LENGTH: 234
 / TYPE: PRT
 / ORGANISM: Homo sapien
 PCT-US03-38808-248

Query Match 98.4%; Score 1181; DB 1; Length 234;
 Best Local Similarity 96.2%; Pred. No. 1.5e-112;
 Matches 225; Conservative 1; Mismatches 0; Gaps 1;

Qy 1 MKMVA[PWTRFYSNSCLCCHVRTGTLGWLILNAVVLILSALADPQYNESSL 60
 Db 1 MKMVA[PWTRFYSNSCLCCHVRTGTLGWLILNAVVLILSALADPQYNESSL 60

Qy 61 GGDFFEMDDANMCIAIAISLMLICAMATYGA[KORAM]IIPFFCYQIFDFALNMLVAI 120

RESULT 4
 PCT-US03-38808-240
 / Sequence 240, Application PC/TUS0338808
 / GENERAL INFORMATION:
 / APPLICANT: diadexus, Inc.
 / APPLICANT: Macina, Roberto
 / APPLICANT: Turner, Leah
 / APPLICANT: Sun, Yongming
 / APPLICANT: Rodriguez, Maria
 / APPLICANT: Tim Burcham
 / TITLE OF INVENTION: Compositions, Splice Variants and Methods Relating to Colon Speci
 / CURRENT APPLICATION NUMBER: PCT/US03/38808
 / CURRENT FILING DATE: 2003-12-04
 / PRIOR APPLICATION NUMBER: US 60/431,133

Query Match 96.8%; Score 1161; DB 1; Length 233;
 Best Local Similarity 97.8%; Pred. No. 1.6e-110;
 Matches 219; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MKMVA[PWTRFYSNSCLCCHVRTGTLGWLILNAVVLILSALADPQYNESSL 60
 Db 1 MKMVA[PWTRFYSNSCLCCHVRTGTLGWLILNAVVLILSALADPQYNESSL 60

Qy 61 GGDFFEMDDANMCIAIAISLMLICAMATYGA[KORAM]IIPFFCYQIFDFALNMLVAI 120
 Db 61 GGDFFEMDDANMCIAIAISLMLICAMATYGA[KORAM]IIPFFCYQIFDFALNMLVAI 120

Qy 121 TVLYPNSI[QEY]TROLPPNPFYRDDMSNPTCLVLILFISITLTFKGYLISCVNNCY 180
 Db 121 TVLYPNSI[QEY]TROLPPNPFYRDDMSNPTCLVLILFISITLTFKGYLISCVNNCY 180

Qy 181 RYINGRNSDVLVYTTSNDT[VL]LPYDDATVNGA[KE]PPPPYV 224
 Db 181 RYINGRNSDVLVYTTSNDT[VL]LPYDDATVNGA[KE]PPPPYV 224

Qy 181 RYINGRNSDVLVYTTSNDT[VL]LPYDDATVNGA[KE]PPPPYV 224
 Db 181 RYINGRNSDVLVYTTSNDT[VL]LPYDDATVNGA[KE]PPPPYV 224

RESULT 5
 PCT-US03-38808-241
 / Sequence 241, Application PC/TUS0338808
 / GENERAL INFORMATION:
 / APPLICANT: diadexus, Inc.
 / APPLICANT: Macina, Roberto
 / APPLICANT: Turner, Leah
 / APPLICANT: Sun, Yongming
 / APPLICANT: Rodriguez, Maria
 / APPLICANT: Tim Burcham
 / TITLE OF INVENTION: Compositions, Splice Variants and Methods Relating to Colon Speci
 / CURRENT APPLICATION NUMBER: PCT/US03/38808
 / CURRENT FILING DATE: 2003-12-04
 / PRIOR APPLICATION NUMBER: US 60/431,133

Query Match 98.4%; Score 1181; DB 1; Length 234;
 Best Local Similarity 96.2%; Pred. No. 1.5e-112;
 Matches 225; Conservative 1; Mismatches 0; Gaps 1;

Qy 1 MKMVA[PWTRFYSNSCLCCHVRTGTLGWLILNAVVLILSALADPQYNESSL 60
 Db 1 MKMVA[PWTRFYSNSCLCCHVRTGTLGWLILNAVVLILSALADPQYNESSL 60

Qy 61 GGDFFEMDD-----ANN[IA]AISLMLICAMATYGA[KORAM]IIPFFCYQIFDF 112

PRIOR FILING DATE: 2002-12-04
 NUMBER OF SEQ ID NOS: 254
 SOFTWARE: PatentIn version 3.1

SEQ ID NO: 241
 LENGTH: 319
 TYPE: PRT
 ORGANISM: Homo sapien
 FEATURE:
 NAME/KEY: MISC_FEATURE
 LOCATION: (2) .
 OTHER INFORMATION: x-any amino acid
 PCT-US03-38808-241

Query Match 95.3%; Score 1144; DB 1; Length 319;
 Best Local Similarity 98.2%; Pred. No. 1.2e-108;
 Matches 216; Conservative 1; Mismatches 0; Gaps 0;

Qy 1 MKMVAAPTRPVSNSCCCLCHVRGTGTLGGWYLINAVVLLLSALDPQYNFSSSL 60
 Db 85 MKMVAAPTRPVSNSCCCLCHVRGTGTLGGWYLINAVVLLLSALDPQYNFSSSL 144

Qy 61 GGDFFEPMDAANCIATAISSILMILICATMAYKORAAWIPPFCCYQDFALNMLVAI 120
 Db 145 GGDFFEPMDAANCIATAISSILMILICATMAYKORAAWIPPFCCYQDFALNMLVAI 204

Qy 121 TVLIYNSIQEYIROLPPNPYRDDMSNPTCLVLIILPISTILTPKGYLISCVNCY 180
 Db 205 TVLIYNSIQEYIROLPPNPYRDDMSNPTCLVLIILPISTILTPKGYLISCVNCY 264

Qy 181 RYNGRNSDVLVYVTSNDTTLPLPYDATINGAKAEP 220
 Db 265 RYNGRNSDVLVYVTSNDTTLPLPYDATINGACQAP 304

RESULT 6
 US-09-614-150A-36129
 Sequence 36129, Application US/09614150A
 GENERAL INFORMATION:
 APPLICANT: Venter, J. Craig
 ATTORNEY/AGENT: et al.
 TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE GENES.

CURRENT APPLICATION NUMBER: US/09/614,150A
 CURRENT FILING DATE: 2000-07-11
 PRIOR APPLICATION NUMBER: 60/157,832
 PRIOR FILING DATE: 1999-10-05
 PRIOR APPLICATION NUMBER: 60/160,191
 PRIOR FILING DATE: 1999-10-19
 PRIOR APPLICATION NUMBER: 60/161,932
 PRIOR FILING DATE: 1999-10-28
 PRIOR APPLICATION NUMBER: 60/164,769
 PRIOR FILING DATE: 1999-11-12
 PRIOR APPLICATION NUMBER: 60/173,383
 PRIOR FILING DATE: 1999-12-28
 PRIOR APPLICATION NUMBER: 60/175,693
 PRIOR FILING DATE: 2000-01-12
 PRIOR APPLICATION NUMBER: 60/184,831
 PRIOR FILING DATE: 2000-02-24
 PRIOR APPLICATION NUMBER: 60/191,637
 PRIOR FILING DATE: 2000-03-23
 NUMBER OF SEQ ID NOS: 43008
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 4479
 LENGTH: 432
 TYPE: PRT
 ORGANISM: DROSOPHILA

US-09-614-150A-4479

Query Match 23.5%; Score 282.5; DB 5; Length 432;
 Best Local Similarity 26.4%; Pred. No. 9.4e-21;
 Matches 68; Conservative 40; Mismatches 97; Indels 53; Gaps 5;

Qy 14 SCCLCHVRGTGTLGGWYLINAVVLLLSALDPQYNFSSSL-GGDFFEPMD--- 69
 Db 39 TCCFGUHVHTATLMLGLWFLNLALSALDPQYNFSSSL-GGDFFEPMD--- 94

Qy 70 -----ANNCIATAISSILMILICATMAYKORAAWII 102
 TYPE: PRT
 ORGANISM: DROSOPHILA

Db 95 PALPPPLSKVPPPYAIRDHSLNRYKRYQNEDMGGLVCTCMIAITMMIYTGKPSHLL 154

Query Match 103.0%; Score 282.5; DB 5; Length 425;
 Best Local Similarity 26.4%; Pred. No. 9.2e-21;
 Matches 68; Conservative 40; Mismatches 97; Indels 53; Gaps 5;

Qy 103 PFFCYQIFDPAALNMVAVTLYIYNPSIQEYIROLPPNPYRDDMSNPTCLVLIILIFI 162
 Db 155 PFFCYQIFDPAITTAAGYLCLYQIAHSTIAE-SHRLPWRKLBPLPPEBLVVLVVF 206

Qy 163 SIIITFGYLISCVWNCYRYI-----INGRNSSDVLYVTSNDTTVILP 205
 Db 214 ICIVFLRKYACIGIVRCKYLTLRQHVRTRLFPEPPTGVSCTGREGAERSYLLP 273

Qy 206 PYDDATVNGAAKEPPFY 223
 Db 274 NYDEATAQYLKQAPPFY 291

RESULT 8
 PCT-US02-41798A-33
 ; Sequence 33, Application PC/TUS0241798A
 ; GENERAL INFORMATION:
 ; APPLICANT: FRANTZ, GRETCHEN
 ; APPLICANT: HILLIAN, KENNETH J.
 ; APPLICANT: PHILLIPS, HEIDI S.
 ; APPLICANT: POLAKIS, PAUL
 ; APPLICANT: SMITH, VICTORIA
 ; APPLICANT: SPENCER, SUSAN D.
 ; APPLICANT: WILLIAMS, P. MICKEY
 ; APPLICANT: WU, THOMAS D.
 ; APPLICANT: ZHANG, ZENIN
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
 ; TITLE OF INVENTION: TREATMENT OF TUMOR
 ; FILE REFERENCE: P5014R1-PCT
 ; CURRENT APPLICATION NUMBER: PCT/US02/41798A
 ; CURRENT FILING DATE: 2002-12-30
 ; PRIOR APPLICATION NUMBER: US 60/345,444
 ; PRIOR FILING DATE: 2002-01-02
 ; PRIOR APPLICATION NUMBER: US 60/351,885
 ; PRIOR FILING DATE: 2002-01-25
 ; PRIOR APPLICATION NUMBER: US 60/360,066
 ; PRIOR FILING DATE: 2002-02-25
 ; PRIOR APPLICATION NUMBER: US 60/362,004
 ; PRIOR FILING DATE: 2002-03-05
 ; PRIOR APPLICATION NUMBER: US 60/366,869
 ; PRIOR FILING DATE: 2002-03-20
 ; PRIOR APPLICATION NUMBER: US 60/366,284
 ; PRIOR FILING DATE: 2002-03-21
 ; PRIOR APPLICATION NUMBER: US 60/368,679
 ; PRIOR FILING DATE: 2002-03-28
 ; PRIOR APPLICATION NUMBER: US 60/404,809
 ; PRIOR FILING DATE: 2002-08-19
 ; PRIOR APPLICATION NUMBER: US 60/405,645
 ; PRIOR FILING DATE: 2002-08-21
 ; NUMBER OF SEQ ID NOS: 95
 ; SEQ ID NO: 33
 ; LENGTH: 262
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 PCT-US02-41798A-33

Query Match 14.6%; Score 175.5; DB 1; Length 262;
 Best Local Similarity 22.8%; Pred. No. 4.2e-10;
 Matches 48; Mismatches 83; Indels 75; Gaps 12;

Qy 14 SCCLCCHVRTSTILLGWLILINAYVLLILSALADPQDNFSSSELGDFEFDANMC 73
 Db 11 TCC-CFNRVRIATTALAIYHIM-SVLLFTEHSVEAHGKASCKLSQMG---YLRIADJ 64

Qy 74 IAIATSLMLIICATMYGAYKORAII-----IPPFCCYQIFPDFALNMVLA-- 119
 Db 40 ---SLQIMDYLCLLTLGSYIPELYAKLRSRASSKFPMLTQLIDFCSLTLLCS 96

Qy 14 SCCLCCHVRTGWLILINAVVLLILSALADPQDNFSSSELGDFEFDANMC 73
 Db 11 TCC-CFNRVRIATTALAIYHIM-SVLLFTEHSVEAHGKASCKLSQMG---YLRIADJ 64

Qy 74 IAIATSLMLIICATMYGAYKORAII-----IPPFCCYQIFPDFALNMVLA-- 119
 Db 40 ---SLQIMDYLCLLTLGSYIPELYAKLRSRASSKFPMLTQLIDFCSLTLLCS 96

Qy 120 -ITVLIYDN-SIOBYIROLP--PNFPYRDDVMSVNPTCLVLLFISIILPKGYLIS 174
 Db 97 SYMEVPTYLNFKSNHHMNYLPSQDMPHNOQF---KMMIIFIAFTYLI-FKYYMFK 150

Qy 175 CWNNGRYTNGRNS-----SDVLYVYTSNDTIVLPPYDATVNGAAKEP---PPY 223
 Db 151 CWWRCYRLIKCMNSVKEKRNSKML-----QKVLPSKTPEGGPAPPY 202

RESULT 9
 PCT-US03-37278-7
 ; Sequence 7, Application PC/TUS0337278
 ; GENERAL INFORMATION:
 ; APPLICANT: INCYTE CORPORATION; EMBERLING, Brooke M.;
 ; APPLICANT: CHIEN, David; WANG, Jonathan T.;
 ; APPLICANT: RICHARDSON, Thomas W.; RAMKUMAR, Jayalaxmi;
 ; APPLICANT: KHARE, Reena; ELLIOTT, Vicki S.;
 ; APPLICANT: LEE, Soo Yean; BHATIA, Umesh G.;
 ; APPLICANT: BURRILL, John D.; LEE, Sally;
 ; APPLICANT: BLAKE, Julie J.; HO, Anne;
 ; APPLICANT: ZHEN, Wenjin
 ; TITLE OF INVENTION: ORGANICELLE-ASSOCIATED PROTEINS
 ; FILE REFERENCE: PF-1621 PCT
 ; CURRENT APPLICATION NUMBER: PCT/US03/37278
 ; CURRENT FILING DATE: 2003-11-21
 ; PRIOR APPLICATION NUMBER: US 60/429,445
 ; PRIOR FILING DATE: 2002-11-26
 ; PRIOR APPLICATION NUMBER: US 60/430,833
 ; PRIOR FILING DATE: 2002-12-03
 ; SOFTWARE: PERL program
 ; SEQ ID NO: 7
 ; LENGTH: 205
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; OTHER INFORMATION: Incyte ID No: 7522328CD1
 PCT-US03-37278-7

Query Match 12.8%; Score 153; DB 1; Length 205;
 Best Local Similarity 22.1%; Pred. No. 6.1e-08;
 Matches 53; Conservative 42; Mismatches 67; Indels 78; Gaps 12;

Qy 14 SCCLCCHVRTGWLILINAVVLLILSALADPQDNFSSSELGDFEFDANMC 73
 Db 11 TCC-CFNRVRIATTALAIYHIM-SVLLFTEHSVEAHGKASCKLSQMG---YLRIADJ 64

Qy 74 IAIATSLMLIICATMYGAYKORAII-----IPPFCCYQIFPDFALNMVLA-- 119
 Db 40 ---SLQIMDYLCLLTLGSYIPELYAKLRSRASSKFPMLTQLIDFCSLTLLCS 96

Qy 120 -ITVLIYDN-SIOBYIROLP--PNFPYRDDVMSVNPTCLVLLFISIILPKGYLIS 174
 Db 97 SYMEVPTYLNFKSNHHMNYLPSQDMPHNOQF---KMMIIFIAFTYLI-FKYYMFK 150

Qy 175 CWNNGRYTNGRNS-----SDVLYVYTSNDTIVLPPYDATVNGAAKEP---PPY 223
 Db 151 CWWRCYRLIKCMNSVKEKRNSKML-----QKVLPSKTPEGGPAPPY 202

RESULT 10
 PCT-US03-37278-7
 ; Sequence 42447, Application US/09614150A
 ; GENERAL INFORMATION:
 ; APPLICANT: Venter, J. Craig
 ; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
 ; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
 ; TITLE OF INVENTION: DROSOPHILA GENES.
 ; FILE REFERENCE: CL000728
 ; CURRENT APPLICATION NUMBER: US/09/614,150A
 ; CURRENT FILING DATE: 2000-07-11
 ; PRIOR APPLICATION NUMBER: 60/157,832
 ; PRIOR FILING DATE: 1999-10-05
 ; PRIOR APPLICATION NUMBER: 60/160,191
 ; PRIOR FILING DATE: 1999-10-19

Qy 14 SCCLCCHVRTSTILLGWLILINAYVLLILSALADPQDNFSSSELGDFEFDANMC 73
 Db 11 TCC-CFNRVRIATTALAIYHIM-SVLLFTEHSVEAHGKASCKLSQMG---YLRIADJ 64

Qy 74 IAIATSLMLIICATMYGAYKORAII-----IPPFCCYQIFPDFALNMVLA-- 119
 Db 40 ---SLQIMDYLCLLTLGSYIPELYAKLRSRASSKFPMLTQLIDFCSLTLLCS 96

Qy 65 SSFLITMLPFIISLISLIGVYKNERKYLPLSLQIMDYLCLLTLGSYI--ELPAVL 121

Qy 134 -----ROLPPNFPYR----DDVMSVNPCTC----- 153

Db 122 KLASRSRASSSKFPMLTQLIDFCSLTLLCSYMBVPTVLNFKSMNHNLYLPSQEDMPH 181

Qy 154 -----LVLILLLFISLITPKGYLISCVWNCYRYNGNS-----SDVLYVYTSNDTIVLPPYDATVNGAAKEP---PPY 201
 Db 182 NQFICMIMIISIAFTVIL-FKVMFKCIVWRCYRJIKCMNSVKEKRNSKML-----QK 233

PRIOR APPLICATION NUMBER: 60/161,932
 PRIOR FILING DATE: 1998-10-08
 PRIOR APPLICATION NUMBER: 60/164,769
 PRIOR FILING DATE: 1999-11-12
 PRIOR APPLICATION NUMBER: 60/173,383
 PRIOR FILING DATE: 1999-12-28
 PRIOR APPLICATION NUMBER: 60/175,693
 PRIOR FILING DATE: 2000-01-12
 PRIOR APPLICATION NUMBER: 60/184,831
 PRIOR FILING DATE: 2000-02-24
 PRIOR APPLICATION NUMBER: 60/191,637
 PRIOR FILING DATE: 2000-03-23
 NUMBER OF SEQ ID NOS: 43008
 SOFTWARE: FastSEQ for Windows Version 4.0
 TYPE: PRT
 ORGANISM: DROSOPHILA
 US-09-614-150A-42447

Query Match Score 10.3%; DB 5; Length 165;
 Best Local Similarity 21.7%; Pred. No. 6.9e-05;
 Matches 40; Conservative 42; Mismatches 56; Indels 46; Gaps 7;
 Db 7 NSCCLCCHVRCITLGVWYLJINAVVLLIUSALADPQYNFSSSELGGDFEFMD--- 69
 Db 7 NSCCLCOSTRNSVSLAIVLVSITIVVIFTT---RTHFKCTI---IFDFIPNDIV 57

Qy 70 ---AMCIAIAISLMLICAMATGAKKORAAMIPPFCCYQIFDFAIMLVAITVLI 124
 Db 58 KIILVNLNCMTLISLMII-----GALKRNHYLMVPW-----VVLGIMIAIGLII 103
 Qy 125 YPNSIGQSYIROLQPNNPFYRDVMSVNPCTLYLII-LLFISITLTFKGYLISCVNCRYI 183
 Db 104 -----SVYTGTGIVFPIDGYVLTGVLWLGIVLCAIMTYCWCVVISEYANL 149

Qy 184 NGRN 187
 Db 150 SEEN 153

RESULT 11-10-415-182A-4106
 Sequence 4106, Application US/10415182A
 GENERAL INFORMATION: The 'Xaa' at location 385 stands for Lys, Asn, Arg, Ser, Thr, Cys, or Phe.
 APPLICANT: Telford, John
 TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
 FILE REFERENCE:
 CURRENT APPLICATION NUMBER: US/10/415,182A
 PRIOR FILING DATE: 2000-10-27
 PRIOR APPLICATION NUMBER: GB-0026333.5
 PRIOR FILING DATE: 2000-11-24
 PRIOR APPLICATION NUMBER: GB-0105640.7
 PRIOR FILING DATE: 2001-03-07
 NUMBER OF SEQ ID NOS: 12024
 SOFTWARE: SeqWin99, version 1.02
 SEQ ID NO: 4106
 LENGTH: 260
 TYPE: PRT
 ORGANISM: Streptococcus agalactiae
 US-10-415-182A-4106

Query Match Score 8.4%; DB 6; Length 260;
 Best Local Similarity 24.0%; Pred. No. 0.016; Mismatches 73; Indels 26; Gaps 6;
 Matches 41; Conservative 31; Mismatches 73; Indels 26; Gaps 6;
 Qy 28 LGVWYLINAVVLLIUSALADPQYNFSSSELGGDFEFMDIAISLMLI 85
 Db 13 VGKWLTLNAAVVLLISLGLV-----KALGGNFS-TDTNSTSAQIFTILVLL 61
 Qy 86 CAMATGAKKORAAMIPPFCCYQIFDFAIMLVAITVLYPNSI--QETYRQLPPNPPYR 143

Db 62 LAMVTSGLSLTAAIIKRSYNSI-FGRGCGYLTLPLVTTNQITCSKLASL----- 112
 Qy 144 DDVMSVNPCTLYLISITLTFKGYLISCVNCRYIINGRNSSDVLY 194
 Db 113 --LNSLFNITVILGILVILPVGIGQFVVAFFPKYKLSSNAPLFAY 161.

RESULT 12-10-726-216-16
 Sequence 16, Application US/10726216
 GENERAL INFORMATION:
 APPLICANT: Nichols, Timothy C.;
 APPLICANT: Malouf, Nadia
 APPLICANT: Merricks, Elizabeth
 TITLE OF INVENTION: Purified and Isolated Platelet Calcium Channel Nucleic Acids and Polypeptides and Therapeutic and Screening Methods Using Same
 FILE REFERENCE: 421/29/2/2
 CURRENT APPLICATION NUMBER: US/10/726,216
 CURRENT FILING DATE: 2005-12-02
 PRIOR APPLICATION NUMBER: US 09/029,413
 PRIOR FILING DATE: 2001-12-20
 PRIOR APPLICATION NUMBER: US 60/258,169
 PRIOR FILING DATE: 2000-12-22
 NUMBER OF SEQ ID NOS: 29
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 16
 LENGTH: 1772
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (383) .. (333)
 OTHER INFORMATION: The 'Xaa' at location 383 stands for Glu, Asp, Gly, Ala, or Val.
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (384) .. (384)
 OTHER INFORMATION: The 'Xaa' at location 384 stands for Lys, Asn, Arg, Ser, Thr, Cys, or Phe.
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (385) .. (385)
 OTHER INFORMATION: The 'Xaa' at location 385 stands for Lys, Asn, Arg, Ser, Thr, Cys, or Phe.
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (386) .. (386)
 OTHER INFORMATION: The 'Xaa' at location 386 stands for Lys, Asn, Arg, Ser, Thr, Cys, or Phe.
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (387) .. (387)
 OTHER INFORMATION: The 'Xaa' at location 387 stands for Lys, Asn, Arg, Ser, Thr, Cys, or Phe.
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (388) .. (388)
 OTHER INFORMATION: The 'Xaa' at location 388 stands for Lys, Asn, Arg, Ser, Thr, Cys, or Phe.
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (389) .. (389)
 OTHER INFORMATION: The 'Xaa' at location 389 stands for Lys, Asn, Arg, Ser, Thr, Cys, or Phe.

Qy 73 CIAIAISLMLICAMATGAYKQRAAWIIPPFYCQIPDFALNMVAVITVLIPNSIQEY 132
 Db 53 8 ---TAIPFVEIL-KMTPFGATLHKGA-----FCRNYFL-LDMLYVGVSIV----- 579
 Qy 133 IRLQPPNPYRDDVMSYNTPLCLVLLILFISLITLTPKG--YLISCVWNCRYINGRNSSD 190
 Db 580 -----SPGIQSSAISVVKILRVLRLVPLAINRAKGLKHVQCVFVAIRTI-----GN 628
 Qy 191 VLVYVT 196
 Db 629 IMIVTT 634
RESULT 13
 US-10-726-216-22
 Sequence 22, Application US/10726216
 GENERAL INFORMATION:
 APPLICANT: Nichols, Timothy C.
 APPLICANT: Malouf, Nadia
 APPLICANT: Merricks, Elizabeth
 TITLE OF INVENTION: Polypeptides and Therapeutic and Screening Methods Using Same
 FILE REFERENCE: 421/29/2/2
 CURRENT APPLICATION NUMBER: US/10/726,216
 CURRENT FILING DATE: 2003-12-02
 PRIOR APPLICATION NUMBER: US 09/029,413
 PRIOR FILING DATE: 2001-12-20
 PRIOR APPLICATION NUMBER: US 60/258,169
 PRIOR FILING DATE: 2000-12-22
 NUMBER OF SEQ ID NOS: 29
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO: 22
 LENGTH: 1873
 TYPE: PRT
 ORGANISM: Oryctolagus cuniculus
 US-10-726-216-22

Query Match 7.9%; Score 95; DB 6; Length 1873;
 Best Local Similarity 24.0%; Pred. No. 0.63; Indels 46; Gaps 9;
 Matches 46; Conservative 31; Mismatches 69; Indels 46; Gaps 9;
 US-10-726-216-22

Qy 12 SNSCCILCCHVTRGTTLGGWVLLINAVVLLLSSBLLGGDFEEM 67
 Db 785 TNKVRVLCH---RIVNATWP---TNFILPILLSSAALAAPIRAESVRNQILGYFD-- 836
 Qy 68 DDANMCTAIAISLMLICAMATGAYKQRAAWIIPPFYCQIPDFALNMVAVITVLIPN 127
 Db 837 -----IAFTSIVETVETLKVMTGATLHKGS----FCRNYFL-LDMLYVGVSIV--- 881
 Qy 128 SIQEYIRQLPPNPYRDDVMSYNTPLCLVLLILFISLITLTPKG--YLISCVWNCRYING 185
 Db 882 -----SMGLESSTISIVKLLRVLRLVPLAINRAKGLKHVQCVFVAIRTI GN 930
 Qy 186 RNSSDVLVYVTS 197
 Db 931 -----IVLVTT 936

RESULT 14
 US-09-614-150A-207
 Sequence 207, Application US/09614150A
 GENERAL INFORMATION:
 APPLICANT: Venter, J. Craig
 APPLICANT: et al.
 TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE GENES.
 TITLE OF INVENTION: DROSOPHILA GENES.
 FILE REFERENCE: CLO00728
 CURRENT APPLICATION NUMBER: US/09/614,150A
 CURRENT FILING DATE: 2000-07-11
 PRIOR APPLICATION NUMBER: 60/157,832
 PRIOR FILING DATE: 1999-10-05
 PRIOR APPLICATION NUMBER: 60/160,191

Query Match 7.6%; Score 91; DB 6; Length 551;
 Best Local Similarity 22.0%; Pred. No. 0.39; Mismatches 32; Indels 46; Gaps 9;
 Matches 37; Conservative 32; Mismatches 53; Indels 46; Gaps 9;
 US-10-614-150A-207

Qy 22 RTGTGTLGGW-YLINAVVLLLSSALADPDQYNRSSSELGGDPFMDANMC-1AIAIS 79
 Db 395 RSQTPLIAVTVYAVLLEIILNLGLA-----SSTAGAVF-----NVCTVALNV 438
 Qy 80 LLMILICAMATGAYKQRAAWIIPPFYCQIPDFALNMVAVITVLIPNSQEYIQLPPN 139
 Db 439 YVIP1CKM-VYGR-MQKGPHWGMGKSYVWVNAFAWNTMVAIIFT----- 482
 Qy 140 FPYRDDVMSYNTPLCLVLLILFISLITLFGYLISCVWNCRYINGRN 187

483 FPTTRVPVTPEMNQYAIFFFFLILALVF-----W-----YTHGRH 518

Search completed: February 2, 2004, 14:28:02
Job time : 26 secs

cannabinoïd receptor
 NADH2 dehydrogenase
 hypothetical protein
 ABC-type transport
 probable permease
 hypothetical protein
 Na+/H+-exchanging
 protein
 AcOrf-124 protein
 DNA transfer protein
 calcium channel, v
 voltage-dependent
 voltage-dependent
 protein B0416.3 [i]
 hypothetical protein
 probable olfactory
 probable membrane
 protein
 cannabinoïd receptor
 GenCore version 5.1.6
 Copyright (c) 1993 - 2004 Compugen Ltd.
 NM protein - protein search, using bw model
 Run on: February 2, 2004, 14:20:15 ; Search time 21 Seconds
 (without alignment(s))
 1034.958 Million cell1 updates/sec
 File: US-09-965-529-26
 Perfect score: 1200
 Sequence: 1 MKRYAPWTRFYSNSCCLCCH.....YDDATVNGAAKEPPPPVSA 226
 Scoring table: BLOSUM62

searched: 283308 seqs, 96168682 residues
 current number of hits containing chosen alignment: 262200

minimum DB seq length: 0
total number of hits satisfying chosen parameters: 282200
RESULT 1
G02476

lysosomal-associated-membrane protein - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision
C:Accession: C02475
C:Version: 06-Jun-1997 #text_change 05-Nov-1999

PIR 76 :*
Database :
Listed first 45 summaries
Last updated March 1996.
R;Liu, B.; Adra, C.N.
Submitted to the EMBL Data Library, March 1996
A;Reference number: H01341

1: pir1: *
2: pir2: *
3: pir3: *
A;Accession: GO2476
A;Status: preliminary; translated from GB/EMBL/DBJ

Pred. No. is the number of results predicted by chance to have a
 4: **pir4:** *

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Best Local Similarity 22.8%; Pred. No. 1.3e-08;
Matches 61; Conservative 48; Mismatches 83; Indels 75; Gaps 12

No.	Score	Match Length	DB	ID	Description	Qy	14
						SCCLCCHVTRGTILLGWWYLINAVYLILLISALADPQDNFSSSELGGDFEFMDANMC 73	SCCLCCHVTRGTILLGWWYLINAVYLILLISALADPQDNFSSSELGGDFEFMDANMC 73

4 98.5 8.2 265 T26217 hypothetical prote
5 96 8.0 151 2 T18949 hypothetical prote

134 - - - - RQLPPNFPYR - - - DDVMSVNPYC - - -
QY

				RESULT 2
19	88	7.3	372	hypothetical prote
20	88	7.3	440	hypothetical prote
21	87.5	7.3	309	hypothetical prote
			24804	T15415

24 87 7.2 639 2 13220 hypothetical, broke
25 87 7.2 639 2 T50793
26 87 7.2 2220 2 A45290 calcium channel pr
C;Accession: T15415
R;Geisel, C.

submitted to the EMBL Data Library, April 1996
 A; Description: The sequence of *C. elegans* cosmid C05E11.
 A; Reference number: 218347

A;Accession: T15415
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-250 <GBI>
 A;Cross-references: EMBL:U53338; NID:gi1255840; PID:gi1255844; PIDN:AAA96192.1; GSPDB:GN00
 A;Experimental source: strain Bristol N2; clone C05E11
 C;Genetics:
 A;Gene: CESP:COSE11.3
 A;Map position: X
 A;Introns: 23/1; 39/3; 97/3; 146/3; 194/1

Query Match 8.5%; Score 102.5; DB 2; Length 250;
 Best Local Similarity 21.9%; Pred. No. 0.055; Mismatches 46; Indels 69; Gaps 12;
 Matches 46; Conservative 46; Hypothetical protein W06B11.3 - *Caenorhabditis elegans*

Qy 16 CLCCHYRTGTLG----WVYLINAVVLLI----LISALADPDQYNESS--SELQG 62
 Db 57 CINCCHYKTAGFLGCVHVNMLFLFLHSLFVYFQHDGRLQQARGVKTNYFGSTLAEMG 116
 Qy 63 DFEFMDAANCIACIATSLMILICAMATGAYKQDAAWH1PFFCYQIFDEA--LNMLVAY 120
 Db 117 -----LGLGIFAVFLFLVALS----RNSALIYVPHLMQVIALCFIVLFC 160
 Qy 121 TVLYPNSTQBY--IRQLP----PNFPRDDVMSYNPTCLV----LITTLEFISIILTPTFG 170
 Db 161 TIALCTDSAYEYRLINAAPPMEHPN----NNTVALDTGTMRVYSLMITYAVSLEF-- 214
 Qy 171 YLISICWNYCERYINGRNNSDYLVYVTSNDT 200
 Db 215 WFIVVYINCNRYLDER--SDYMKYCLAFFT 242

RESULT 3
 S52673 probable membrane protein YDR107c - yeast (*Saccharomyces cerevisiae*)
 N;Alternate names: hypothetical protein YDR107.03C
 C;Species: *Saccharomyces cerevisiae*
 C;Date: 19-May-1995 #sequence_revision 01-SEP-1995 #text_change 19-Apr-2002
 C;Accession: S52673
 R;Murphy, L.; Shore, L.; Harris, D.
 Submitted to the EMBL Data Library, March 1995
 A;Reference number: S52671
 A;Accession: S52673
 A;Molecule type: DNA
 A;Residues: 1-672 <MUR>
 A;Cross-references: EMBL:Z448758; NID:gi747879; PID:gi747882; GSPDB:GN00004; MIF5:YDR107C
 A;Gene: MIF5:YDR107C
 A;Cross-references: SGD:S0002514
 C;Keywords: Schizosaccharomyces pombe probable transmembrane protein SPBC1105.08
 C;Genetics:
 P;1:311-327/Domain: transmembrane #status predicted <TM1>
 P;1:384-400/Domain: transmembrane #status predicted <TM2>
 P;1:408-424/Domain: transmembrane #status predicted <TM3>
 P;1:441-460/Domain: transmembrane #status predicted <TM4>
 P;1:479-495/Domain: transmembrane #status predicted <TM5>
 P;1:536-552/Domain: transmembrane #status predicted <TM6>
 P;1:618-634/Domain: transmembrane #status predicted <TM7>
 P;1:640-656/Domain: transmembrane #status predicted <TM8>

Query Match 8.3%; Score 99.5; DB 2; Length 672;
 Best Local Similarity 20.3%; Pred. No. 0.26; Mismatches 44; Indels 54; Gaps 11;
 Matches 42; Conservative 44; Hypothetical protein C05C12.6 - *Caenorhabditis elegans*

Qy 31 WYLINAVVLLIISAL----ADPQYNESSSELGGDDEBFMDDA----- 70
 Db 310 WFSLNFSVILSSVWHSLLRAKSLDIARY---EYNLNEPHEHSWGLKGHDYF 365
 Qy 71 ----NMCIATAI----SLMILICAM--ATYGAVKQRAAWH1PFFCYQIFDEA-- 113
 Db 366 RTPSKSMLLSTLVSGMQLFIMVMCSIFFAAVGLVSPVSRGLSLPTVYALFGFVGSY 425

C;Superfamily: Caenorhabditis elegans hypothetical protein C05C12.6

Query Match 8.0%; Score 96; DB 2; Length 151;
 Best Local Similarity 22.8%; Pred. No. 0.13;
 Matches 26; Conservative 19; Mismatches 35; Indels 34; Gaps 3;
 Qy 16 CLC--CHVRGRTTLLGWWYLINAVVLLLSSALADPQDYNQSSSELGGDFEPMDDANM 73
 Db 14 CPGCICHVGTGTCQCLWVTTTSAASLRLRMRSS----- 46
 Qy 74 IAIASLMLIC--AMATGAYKORAMWIPPFCCYQIDPFLAMNLVAITVLY 125
 Db 47 ---TCTWLIVPICVVGGLGYAFYSKRHKPFLYFLITVQQLVCMILMATTITF 97

RESULT 6

T20043
 hypothetical protein C49A1.10 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C;Accession: T20043

R;Matthews, L.
 Submitted to the EMBL Data Library, December 1999
 A;Reference number: Z19217

A;Accession: T20043
 A;Species: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-308 <WIL>
 A;Cross-references: EMBL:Z83221; PIDN:CAB05703.1; GSPDB:GN00019; CESP:C49A1.10
 A;Experimental source: clone C49A1
 C;Genetics:
 A;Gene: CESP:C49A1.10
 A;Map position: 1
 A;Introns: 62/2; 81/1; 99/3; 223/1; 254/2

Query Match 7.9%; Score 95; DB 2; Length 308;
 Best Local Similarity 21.0%; Pred. No. 0.32;
 Matches 43; Conservative 41; Mismatches 77; Indels 44; Gaps 9;

Qy 17 LCCHYRTGTTLLGWWYLINAVVLLLSSALADPQDYNQSSSELGGDFEPMDDANM 65
 Db 50 LCSHTPHTRFLRG--YL----CALLSSEGKNPKEFSSFYQBIIMAKYVPCNSNLKLLP 102
 Qy 66 ----FMDDANMCTIAIASLMLICAMATGAYKORAMWIPPFCCYQFDPALMNLVAI 120
 Db 103 SQKSFLQTAGLWVAV---VELFLCALAVYGLFNFLFGNSYNTWFLGLGIISVFLII 158
 Qy 121 TVLIYPNSTQ-EYTRQLPNPYRDDVMWSYNTPLCLVLIILFISILTFKGYLLSCVNC 179
 Db 159 AIAFLVYIAKSENARLWPH-----LQAQFLVFLILVAVIA---ILMLFGA 204
 Qy 180 YRYINGRNSSPDVLYVYTSNDPTVIL 204
 Db 205 YRGII-RNLQGSNTYMSDDSTFL 227

RESULT 7

A30063
 dihydropyridine receptor rabbit
 C;Species: Oryctolegus cuniculus (domestic rabbit)
 C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 24-Nov-1999
 R;Accession: A30063
 R;Tanabe, T.; Takeshima, H.; Mikami, A.; Flockerzi, V.; Takahashi, H.; Kangawa, K.; Kojii
 Nature 328, 313-318, 1987
 A;Title: Primary structure of the receptor for calcium channel blockers from skeletal mu
 A;Reference number: A30063; PMID:87258269;
 A;Accession: A30063
 A;Molecule type: tRNA
 A;Residues: 1-1873 <TAN>
 A;Cross-references: GB:05921; NID:91547; PIDN:CAA29355.1; PMID:91548
 C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain
 C;Keywords: phosphoprotein; transmembrane protein

Query Match 7.9%; Score 95; DB 2; Length 1873;
 Best Local Similarity 24.0%; Pred. No. 1.8;
 Matches 46; Conservative 31; Mismatches 69; Indels 46; Gaps 9;
 Qy 12 SNSCCLCCHVRTGTTLLGWWYLINAVVLLLSSALADPQDYNQSSSELGGDFEPM 67
 Db 785 TNKVRVLCH---RIVNATWF--TNFILFLILSSAALAAEDPIRAESVRNQQLGYFD-- 836
 Qy 68 DDAANMCIAIASLMLICAMATGAYKORAMWIPPFCCYQFDFALMNLVAITVLYFN 127
 Db 837 -----IAFTSVPTVETIYKMTYGAFLHKGS----FCRNVFNI-LDILVVAVSLI-- 881
 Qy 128 SIEQYIRQLPPNPYRDDVMWSYNTPLCLVLIILFISILTFKGYLLSCVNCYRYING 185
 Db 882 -----SMGLESSTIVVYKILRVTAVRPLRAINRAKGKLUHVQQCVFVAIRTIGN 930

RESULT 8

T15755
 hypothetical protein C39D10.6 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
 C;Accession: T15755
 R;Minx, P.
 Submitted to the EMBL Data Library, October 1995
 A;Description: The sequence of C. elegans cosmid C39D10.
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-240 <MIN>
 A;Cross-references: EMBL:U39678; NID:91049439; PIDN:91049444; PIDN:AAA80422.1; CESP:C39D10
 A;Accession: T15755
 A;Genetics:
 A;Gene: CESP:C39D10.6
 A;Introns: 44/3; 79/2; 109/3; 168/1; 192/3
 Query Match 7.9%; Score 94.5; DB 2; Length 240;
 Best Local Similarity 17.0%; Pred. No. 0.28;
 Matches 39; Conservative 49; Mismatches 93; Indels 49; Gaps 7;
 Qy 16 CLC--CHYRTGTTLLGWWYLINAVVLLLSSALADPQDYNQSSSELGGDFEPMDDANM 73
 Db 36 CLCQOLHKKGARIVAIYLNVLPVNI-----FSPTRSSTTVFVY---TC 77
 Qy 74 IAIASLMLICAMATGAYKORAMWIPPFCCYQFDPALMNLVAI 121
 Db 78 MSTATFS--IVIFQSLLPFGVWKKRLYDYPFLQVSISLIVLPI 134
 Qy 122 VLIYPSIOEYIROLPPNPYRDDVMWSYNTPLCLVLIILFISILTFKGYLLSCV 176
 Db 135 FLISIAVGASMVIDLARNGVNTDASQEKLDAALFLVFLCLGLLQYFAEVII 194
 Qy 177 WNCYRYINGRNSSPDVLYVYTSNDPTVIL 226
 Db 195 YSFHNPFLDRENSFFSHFPEYSNS-----AFGSEATPTPPPTYPEA 235

RESULT 9

T21308
 hypothetical protein F23D12.1 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
 C;Accession: T21308
 R;Barlow, K.
 Submitted to the EMBL Data Library, April 1996
 A;Reference number: Z19404
 A;Accession: T21308
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA

A;Residues: 1-301 <WIL>
 A;Cross-references: EMBL:Z71186; PIDN:CAA94913.1; GSDB:GN00028; CESP:F23D12.1
 A;Experimental source: clone F23D12

C;Genetics: A;Gene: CESP:F23D12.1

A;Map position: X

A;Introns: 55/1; 83/2; 109/3; 135/2; 181/3; 211/1; 225/3

Query Match 7.8%; Score 93.5; DB 2; Length 301;
 Best Local Similarity 22.6%; Pred. No. 0.43; Gaps 6;
 Matches 38; Conservative 32; Mismatches 65; Indels 33; Gaps 6;

Db 144 SCCLCCHVRRGTTILGWYLINAVLILL---SALLDPDQYNFSSSBLGGDPFEMDD 69

Db 28 SC--CCHAKTETTIFGIFEFPTICLPAVILQVTRVQDKLSDTESSSLDFHEPEPI 85

Qy 70 ANMCIAAI-----SLLMILICAMATYGAJKORAAWIIPPFYCQIFDFALNMV 118

Db 86 KNAVAYVSSLCHNNIFCFPWAIIQQLLSVDDMFYGIKTIIFWPFPHFIRIIICLICV 145

Qy 119 AITVLYPNSIQEYTRQLLPNPFYRDDVMS-VNPPTCLVTLJILLPISTI 165

Db 146 DAWLIFRAAS-----GTTDDMWSYITP--IVIIAVAVGVI 178

RESULT 10
 S41786

probable sugar transport protein 2 - thermophilic bacterium RTB.B4

N;Alternate names: hypothetical protein 2

C;Species: thermophilic bacterium RTB.B4

C;Date: 07-Sep-1994 #sequence_revision 14-Feb-1997 #text_change 20-Aug-1999

R;Derived: P.P. Gibbs, M.D.i. Bergquist, P.L.

Submitted to the EMBL Data Library, October 1993

A;Description: Cloning, sequencing and over expression of a multifunctional xylanase gene

A;Reference number: S41785

A;Accession: S41786

A;Molecule type: DNA

A;Residues: 1-275 <DWI>

C;Cross-references: EMBL:L188965; PIDN:9311105; PIDN:AA842042.1; PIDN:93111087

C;Superfamily: maltose transport protein malG

Query Match 7.7%; Score 92.5; DB 2; Length 275;
 Best Local Similarity 22.3%; Pred. No. 0.49; Gaps 9;
 Matches 53; Conservative 33; Mismatches 69; Indels 83; Gaps 9;

Db 26 ILLGWYLINAVLILL-----ADPDQYNFSSSLLGGDPFEMDDA 70

Db 13 IFLAWTLIADVPFLMFTSFKTQSELSSGTNTQIPRQPTGNFSTVLEGNPFTYL-K 70

Qy 71 NMCIATAISLIML-ICAMATYGAJKORAAWIIPPFYCQIFDFALN-----MVA 119

Db 71 NSVIAVSISSVLILLSSM-----FAPRFKFAFLNLLIYSLIAGMAP 116

Qy 120 ITVLYP-----NSIQ-----EXTRQLPNPFYRDDVNS 149

Db 117 IHTVLIPIYVLTNKKLYDVTVALIGPYVALSPMSIIFLTPEERAKTC 176

Qy 150 NPTCLVLIILPIS--IILTFKGYLISCVNCRYINGNNSDVLYVTTSDNTVLLP 205

Db 177 SMFRYSDLILPLSAPALITYWINGTYLWNEFVP-----ALVLTSSPFRLLP 225

RESULT 11
 H87470

AcRb/AcrD/AcrF family protein [imported] - Caulobacter crescentus

C;Species: Caulobacter crescentus

C;Accession: H87470

C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001

R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.

B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwin, M.L.; Haft, D.H.; Kolon

n., J.; Birmolaha, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

RESULT 13
 AH1762

A;Title: Complete Genome Sequence of Caulobacter crescentus.

A;Reference number: A87249; MURID:21173698; PMID:11259647

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1032 <STO>

A;Cross-references: GB:AE005673; NID:913423218; PIDN:AAK23764.1; GSDB:GN00148

C;Genetics: A;Gene: C1788

Query Match 7.6%; Score 91.5; DB 2; Length 1032;

Best Local Similarity 24.4%; Pred. No. 2.1;

Matches 42; Conservative 21; Mismatches 72; Indels 37; Gaps 7;

Db 59 ELGGDEFMDANCMICATAISLIMLICAMATYGAJKORAAWI-----PF 104

Db 844 EMGSISIEEAGKANKALAVTFPLMFLMMWVIFQVRSISAMMNVNLATPLALVGAPTL 903

Qy 105 FCYQIFDF ALANMLVAVITLIVPNSI---QEYTRQLPNPFY--RDDVMSVNPCTLV 155

Db 904 IFFOPFGTVAUQGILAGLIMNSLILJGQIQNQEGLDPTPHAVVBTQARPVLT 963

Qy 156 LILFLISITLTFKGYLISCVN-----CTRYINGNSDVLVYVTSNDTLLP 205

Db 964 ALAAVFAFPLT---LSVFWSSMAYTLLGGTGTIL-----TIVFLP 1003

RESULT 12

T14245

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - dermatophytic fungus (Trichophyton rubrum

C;Species: mitochrondrion Trichophyton rubrum

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002

C;Accession: T14245

Ride Biavre, C.; Dujon, B.

Submitted to the EMBL Data Library, November 1998

A;Description: Organisation of the mitochondrial genome of Trichophyton rubrum, part III

A;Reference number: Z17938

A;Accession: T14245

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-343 <DBB>

A;Cross-references: ENBL:Y18476; PIDN:CAA77189.1

A;Experimental source: isolate IP 1817.89

C;Keywords: membrane-associated complex; mitochondrion

A;Genome: SG3

A;Genetic code: SG3

A;Molecule type: DNA

A;Accession: SG3

Query Match 7.6%; Score 91; DB 2; Length 343;

Best Local Similarity 21.7%; Pred. No. 0.83;

Matches 47; Conservative 45; Mismatches 67; Indels 58; Gaps 12;

Db 9 RFYSNSCCUCLCHVRYTGTLLG-----VWYLI-INAVALILLISALADPDQYNSSSE 59

Db 153 FDF-----TLLVLTGFSNLNTTIESQRVVFYFLPLIFLFIGCIAETNAPFDIA 208

Qy 157 ILLFISITLTFKGYLISCVN-----MILICAMATYGAJKORAAWIIPFCYQI 109

Db 209 AESELVSFSMTIESAIFMIFLQAYASIVLICLSSVLFGGYLN---TLLPLNTNV 264

Qy 110 FDF-----AUNMLVAVTLYLTPNSIQEYTRQLPNPFYRDLMSVCFWTL 156

Db 265 CDPNSLFSDYDLYNGLSSUNLAIKTAFLIF--VPIWTRASFPRIRF-DQLMSSVCFWTL 320

Qy 158 ILLFISITLTFKGYLISCVN-----CYRYINGNSDVLVYVTSNDTLLP 193

Db 321 ITAYV-----VLLP-----VIGLNSSLLI 343

hypothetical protein lin2645 [Imported] - <i>Listeria innocua</i> (strain Clip1162)	Db	925 -TAIFTVBILL-KMTTGAFLKGKA----FCRNPFNL-LDMLVVGSLV-----	966
C;Species: <i>Listeria innocua</i>			
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001			
C;Accession: AHA1762			
R;Glaeser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, H.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgeot, O.; Entian, K.D.; Fsihi, H.; D.J. Jones, L.M.; Karst, U.			
Science 294, 849-852, 2001			
A;Authors: Kieft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlutert, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A; Reference number: AB1077; MUID:21537279; PMID:11679669			
A;Accession: AHA1762			
A;Status: preliminary			
A;Molecule type: DNA			
A;Residues: 1-391 <GLA>			
A;Experimental source: strain Clip11626			
C;Genetics:			
A;Gene: lin2645			
Query Match 7.4%; Score 89; DB 2; Length 391;			
Best Local Similarity 18.3%; Fred. No. 14; Mismatches 106; Indels 92; Gaps 11;			
Matches 54; Conservative 43; Mismatches 106; Indels 92; Gaps 11;			
1 MRMVAPW---TRFYSNSCCCLCCHVRGTTILGV----WYIJINAVYLII-----LSA 46	Qy	1 MRMVAPW---TRFYSNSCCCLCCHVRGTTILGV----WYIJINAVYLII-----LSA 46	
44 I SIYSPWLEKNNFGVSSLRFLVLSSLTTLGFSMVIEWLNAVACFLIVGMRLLS 103	Db	44 I SIYSPWLEKNNFGVSSLRFLVLSSLTTLGFSMVIEWLNAVACFLIVGMRLLS 103	
47 LA-----DPOQYNSSSESSSELGGDPERMDAMCIAAISLAMILICAMAT 90	Qy	47 LA-----DPOQYNSSSESSSELGGDPERMDAMCIAAISLAMILICAMAT 90	
104 TAFTIGITSLIYFCYXFYDNLSPPTNLEFTYDAITIDNPNISMPLLLAIIFLVFAFLIQ 163	Db	104 TAFTIGITSLIYFCYXFYDNLSPPTNLEFTYDAITIDNPNISMPLLLAIIFLVFAFLIQ 163	
91 Y-----GAYKOBAAWITP-----PFCYQFDFAFLNMLV 118	Qy	91 Y-----GAYKOBAAWITP-----PFCYQFDFAFLNMLV 118	
164 YTSAKNPKSPSUSRKSKRGKLVSPQRKGLWPFVLPVNPVPTGSESYS 223	Db	164 YTSAKNPKSPSUSRKSKRGKLVSPQRKGLWPFVLPVNPVPTGSESYS 223	
119 AITVLLYPPNSIQEYIRQLPPPFYPRDDVMSVNPCTCLVLIIL----FISIILTPTPKGYLI 173	Qy	119 AITVLLYPPNSIQEYIRQLPPPFYPRDDVMSVNPCTCLVLIIL----FISIILTPTPKGYLI 173	
224 LILPLPFIGDQOQVQALPBEASKK---IAVQVTTLATIAGLIGIVMVLTLFAFMP 280	Db	224 LILPLPFIGDQOQVQALPBEASKK---IAVQVTTLATIAGLIGIVMVLTLFAFMP 280	
174 SCV---WNCYRYINGRNSSDVIVVITSDTTLP---PYDDATNGAAKEPPP 221	Qy	174 SCV---WNCYRYINGRNSSDVIVVITSDTTLP---PYDDATNGAAKEPPP 221	
281 AVIGRFWISYRHYSSEQ-----LILPKRKGPPQDPGLVVLGAREBTP 320	Db	281 AVIGRFWISYRHYSSEQ-----LILPKRKGPPQDPGLVVLGAREBTP 320	
RESULT 14			
A46227			
voltage-dependent Ca2+ channel alpha 1-subunit - golden hamster			
C;Species: <i>Mus musculus</i> auratus (Golden hamster)			
C;C_Dtt: 27-Oct-1993 #sequence_revision 18-Nov-1994 #text_change 11-Jan-2000			
C;Accession: A46227			
R;Faney, G.C.; Wheeler, M.B.; wei, X.; Perez-Reyes, E.; Birnbaumer, L.; Boyd III, A.E.; Boyd, M. Endocrinol. 6, 2143-2152, 1992			
A;Title: Cloning of a novel alpha 1-subunit of the voltage-dependent calcium channel from <i>NCBI</i> backbone (NCBIP:123692)			
A;Status: preliminary; not compared with conceptual translation			
A;Molecule type: mRNA			
A;Residues: 1-1610 <YAN>			
A;Experimental source: insulin-secreting cell line HIT-T15			
A;Note: sequence extracted from <i>NCBI</i> backbone (NCBIP:123692)			
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain			
Query Match 7.4%; Score 88.5; DB 2; Length 1610;			
Best Local Similarity 25.0%; Fred. No. 6; Mismatches 61; Indels 43; Gaps 10;			
Matches 46; Conservative 34; Mismatches 61; Indels 43; Gaps 10;			
75 ATAISLMLILICAMATGAYKQRAAWIIPPFQYQIFDPAFLNMLVATIYLIPNSIQEYIR 134	Qy	75 ATAISLMLILICAMATGAYKQRAAWIIPPFQYQIFDPAFLNMLVATIYLIPNSIQEYIR 134	
874 IRVGCHHLINHIFTNLVFLMSSAIAAEPIRSISFRNTLGYFYAF-----	Db	874 IRVGCHHLINHIFTNLVFLMSSAIAAEPIRSISFRNTLGYFYAF-----	925
926 -TAIFTVBILL-KMTTGAFLKGKA----FCRNPFNL-LDMLVVGSLV-----	Qy	926 -TAIFTVBILL-KMTTGAFLKGKA----FCRNPFNL-LDMLVVGSLV-----	967
135 QLPNNPFYPRDDVMSVNPCTCLVLIIL----FISIILTPTPKGYAF-----	Db	135 QLPNNPFYPRDDVMSVNPCTCLVLIIL----FISIILTPTPKGYAF-----	192
968 ---SFGIQSSAISVVKILVRLVRPLRAINRAKGKXHVQCVFAIRI----GNIM 1018	Qy	968 ---SFGIQSSAISVVKILVRLVRPLRAINRAKGKXHVQCVFAIRI----GNIM 1018	
193 VYVT 196	Db	193 VYVT 196	
1019 IVTT 1022	Qy	1019 IVTT 1022	

Search completed: February 2, 2004, 14:23:44
Job time : 24 secs

Result No.	Score	Query	Match	Length	DB	ID	Description
1	553.5	46.1	233	1	MTRP_HUMAN	Q15012	Q15012 homolog (ortholog), human
2	541.5	45.1	233	1	MTRP_MOUSE	Q60961	Q60961 mouse
3	175.5	14.6	262	1	LAMS_HUMAN	Q15571	Q15571 human
4	156.0	13.0	261	1	LAMS_MOUSE	Q61168	Q61168 mouse
5	95.9	7.9	1873	1	CCAS_RABBIT	P07293	P07293 oryctolagus cuniculus
6	93.9	7.8	1146	1	CCAS_RAT	Q02485	Q02485 rat
7	92.5	7.7	275	1	YOR2_CALSR	P40980	P40980 yeast cell wall protein
8	91.9	7.6	343	1	NULM_TRIUR	Q92238	Q92238 trichophyton rubrum
9	91.9	7.6	551	1	AAPI2_NEUCR	Q59942	Q59942 neurospora crassa
10	89.8	7.4	297	1	T2R4_MOUSE	Q91kt3	Q91kt3 mus musculus
11	88.5	7.4	1610	1	CCAD_MESU	Q99244	Q99244 mesocricetus auratus
12	88.5	7.4	2161	1	CCAD_HUMAN	P27732	P27732 rattus norvegicus
13	88.5	7.4	2203	1	CCAD_RAT	P29867	P29867 drosophila melanogaster
14	88.5	7.3	274	1	NUTM_DROMA	P38680	P38680 neurospora crassa
15	87.5	7.3	470	1	MTR_NEUDR	Q13936	Q13936 homo sapiens
16	87.5	7.2	2221	1	CCAC_HUMAN	P29868	P29868 drosophila melanogaster
17	85.5	7.1	274	1	NUTM_DROS	P29869	P29869 drosophila melanogaster
18	85.5	7.1	274	1	ND2M_DROS	P32802	P32802 saccharomyces cerevisiae
19	85.5	7.1	667	1	EM70_YEAST	P47936	P47936 mus musculus
20	85.5	7.1	347	1	CB2R_MOUSE	P41679	P41679 autographa californica
21	83.9	6.9	247	1	Y124_NEUCA	Q13698	Q13698 homo sapiens
22	83.9	6.9	1873	1	CCAC_HUMAN	Q01815	Q01815 mus musculus
23	83.9	6.9	2139	1	CCAC_MOUSE	Q101071	Q101071 caenorhabditis elegans
24	82.5	6.9	210	1	YT43_GAEB	Q15519	Q15519 homo sapiens
25	82.5	6.8	313	1	OIC1_HUMAN	P48906	P48906 hansemia watanabei
26	81.5	6.8	567	1	NUTM_HANWI	P05609	P05609 methanococcus
27	81.5	6.8	201	1	PBS_METJA	Q35214	Q35214 mus musculus
28	81.5	6.8	337	1	OBST_MOUSE	P03896	P03896 drosophila melanogaster
29	81.5	6.8	341	1	NUTM_DROMB	Q37381	Q37381 acanthocephala
30	80.8	6.8	344	1	NULM_CYACA	P48899	P48899 cyanidium cyanescens
31	80.8	6.7	369	1	NUSC_LIGVU	Q91ta3	Q91ta3 ligustrum vulgare
32	80.8	6.7	738	1	CCAC_RABBIT	P15381	P15381 oryctolagus cuniculus

ALIGNMENTS							
RESULT 1							
MTRP_HUMAN	STANDARD;	PRT;	233 AA.				
ID_MTRP_HUMAN							
AC_Q15012;							
DT_15-JUL-1998 (Rel. 36, Created)							
DT_15-JUL-1998 (Rel. 36, Last sequence update)							
DT_15-SEP-2003 (Rel. 42, Last annotation update)							
DB_Lysosomal-associated transmembrane protein 4A (Golgi 4-transmembrane spanning transporter MTP).							
DB_LAMP4A OR MTRP OR KIAA0108.							
GN_Homo sapiens (Human).							
OC_Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.							
NCBI_TaxID=9606;							
[1]							
RN_RP_SEQUENCE FROM N.A.							
RC_TISSUE=Bone marrow;							
RX_MEDLINE=9330835; PubMed=7788527;							
RA_Nagase T., Miyajima N., Tanaka A., Sazuka T., Seki N., Sato S.,							
RA_Tabata S., Ishikawa K.-I., Kawarabayashi Y., Kotani H., Nomura N.;							
RA_RT_Prediction of the coding sequences of unidentified human genes. III. The coding sequences of 40 new genes (KIAA0081-KIAA0130) deduced by analysis of cDNA clones from human cell line KG-1.";							
RA_RT_analyses of cDNA clones from human cell line KG-1.";							
RA_RT_deduced by analysis of the total score being printed, and is derived by analysis of the total score distribution.							
SUMMARIES							
Result No.	Score	Query	Match	Length	DB	ID	
1	553.5	46.1	233	1	MTRP_HUMAN	Q15012	Q15012 homolog (ortholog), human
2	541.5	45.1	233	1	MTRP_MOUSE	Q60961	Q60961 mouse
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9	91.9	7.6	551	1	AAPI2_NEUCR	Q59942	Q59942 neurospora crassa
10	89.8	7.4	297	1	T2R4_MOUSE	Q91kt3	Q91kt3 mus musculus
11	88.5	7.4	1610	1	CCAD_MESU	Q99244	Q99244 mesocricetus auratus
12	88.5	7.4	2161	1	CCAD_HUMAN	P27732	P27732 rattus norvegicus
13	88.5	7.4	2203	1	CCAD_RAT	P29867	P29867 drosophila melanogaster
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19	85.5	7.1	667	1	EM70_YEAST	P47936	P47936 mus musculus
20	85.5	7.1	347	1	CB2R_MOUSE	P41679	P41679 autographa californica
21	83.9	6.9	247	1	Y124_NEUCA	Q13698	Q13698 homo sapiens
22	83.9	6.9	1873	1	CCAC_HUMAN	Q01815	Q01815 mus musculus
23	83.9	6.9	2139	1	CCAC_MOUSE	Q101071	Q101071 caenorhabditis elegans
24	82.5	6.9	210	1	YT43_GAEB	Q15519	Q15519 homo sapiens
25	82.5	6.8	313	1	OIC1_HUMAN	P48906	P48906 hansemia watanabei
26	81.5	6.8	567	1	NUTM_HANWI	P05609	P05609 methanococcus
27	81.5	6.8	201	1	PBS_METJA	Q35214	Q35214 mus musculus
28	81.5	6.8	337	1	OBST_MOUSE	P03896	P03896 drosophila melanogaster
29	81.5	6.8	341	1	NUTM_DROMB	Q37381	Q37381 acanthocephala
30	80.8	6.8	344	1	NULM_CYACA	P48899	P48899 cyanidium cyanescens
31	80.8	6.7	369	1	NUSC_LIGVU	Q91ta3	Q91ta3 ligustrum vulgare
32	80.8	6.7	738	1	CCAC_RABBIT	P15381	P15381 oryctolagus cuniculus

RESULT 1

MTRP_HUMAN

ID_MTRP_HUMAN

AC_Q15012;

DT_15-JUL-1998 (Rel. 36, Created)

DT_15-JUL-1998 (Rel. 36, Last sequence update)

DT_15-SEP-2003 (Rel. 42, Last annotation update)

DB_Lysosomal-associated transmembrane protein 4A (Golgi 4-transmembrane spanning transporter MTP).

DB_LAMP4A OR MTRP OR KIAA0108.

GN_Homo sapiens (Human).

OC_Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;

RN_RP_SEQUENCE FROM N.A.

RC_TISSUE=Muscle;

RX_MEDLINE=2338827; PubMed=12477932;

RA_Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins P.S., Wagner L., Shemesh C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marszina K., Farmer J.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Logue N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villaldon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahay J., Helton B., Kettman M., Madan A., Rodriguez S., Sanchez A., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallius D.E., RA_Schwarz A., Schein J.B., Jones S.J.M., Marrs M.A., RT_Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.;

RA_Raha S.S., Logue N.A., Peters G.J., Abramson R.D., Mullahy S.J., RA_Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA_Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA_Villaldon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., RA_Fahay J., Helton B., Kettman M., Madan A., Rodriguez S., Sanchez A., RA_Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C., RA_Raha S.S., Logue N.A., Peters G.J., Abramson R.D., Mullahy S.J., RA_Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA_Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallius D.E., RA_Schwarz A., Schein J.B., Jones S.J.M., Marrs M.A., RT_Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.;

RL_Proc. Natl. Acad. Sci. U.S.A. 91:16899-16903 (2002).

CC_-1- FUNCTION: MAY FUNCTION IN THE TRANSPORT OF NUCLEOSIDES AND/OR NUCLEOSIDE DERIVATIVES BETWEEN THE CYTOSOL AND THE LUMEN OF AN INTRACELLULAR MEMBRANE-BOUND COMPARTMENT (BY SIMILARITY).

CC_-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MAY RESIDE IN AN INTRACELLULAR MEMBRANE-BOUND COMPARTMENT (POTENTIAL).

CC_-1- DOMAIN: THE C-TERMINAL DOMAIN IS NECESSARY FOR RETENTION WITHIN INTRACELLULAR MEMBRANES (BY SIMILARITY).

Query Match 13.0%; Score 156; DB 1; Length 261;
 Best Local Similarity 22.4%; Pred. No. 1.2e-06;
 Matches 60; Conservative 48; Mismatches 82; Indels 78; Gaps 13;

Qy 14 SCCLCCHVRGTTLGLWVLLINAVVLLILSALADPQDNFSSESSSELGGDFREFMDANMC 73
 Db 11 TCC-CFNIKVATIALAIYHIMS---VLFLEHHV----EVARKVSRERFKNPYLRNA 61
 Qy 74 IAIASL---MILICAMATGAYKORAAWLIIFCQFEDFALNMVLAVTIVLPPNSIQ 130
 Db 62 DLSSPLIGVFIISLISLGFVVKRNREKYLPSLQIMDCLLITLIGSYI---ELP 118
 Qy 131 EXIROLPPN-FPYRDVMSVY-PTCLVILL----- 160
 Db 119 AYLKLRPRPESPKVPLMTCQLLDFSLISLTLQSSMVEPTYNFKSMNMNYLPSQBSV 178
 Qy 161 ---FISILTF-----KGYLISCVNCCRYINGRNSSDVIVYTSNDTT---- 201
 Db 179 PHSQFINMMLIFSVAFITVLLKVMFKCVYTCKFLKRNNSA-----MEDSSKMEPL 231
 Qy 202 -VLLPPYDATINGAAKEP----PPPY 223
 Db 232 KVALPSYEA-LSLPPKTPPEGDPAPPY 258

RESULT 5

CCAS_RABBIT STANDARD PRT; 1873 AA.
 AC P07283; DT 01-APR-1988 (Rel. 07, Created)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Voltage-dependent L-type calcium channel alpha-1S subunit (Calcium
 DE channel, L type, alpha-1 type, alpha-1S polypeptide, isoform 3, skeletal muscle).
 GN CACNA1S OR CACNA1S3 OR CACNL1A3
 OS Oryctolagus cuniculus (Rabbit).
 OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC NCBITaxID=9986; OX
 RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 TISSUE=Skeletal muscle; RC
 MEDLINE=87258269; PubMed=3037387;
 RA Tanabe T., Takeshima H., Mikami A., Flockerzi V., Takahashi H.,
 RA Kangawa K., Kojima M., Matsuo H., Hirose T., Numa S.,
 RT "primary structure of the receptor for calcium channel blockers from
 RT skeletal muscle.";
 RL Nature 328:313-318 (1987).
 RN SEQUENCE FROM N.A.
 TISSUE=Skeletal muscle;
 MEDLINE=88336904; PubMed=2458626;
 RA Ellis S.B., Williams M.E., Ways N.R., Brenner R., Sharp A.H.,
 RA Leung A.T., Campbell K.P., McKenna E., Koch W.J., Hui A., Schwartz A.,
 RA Harpold M.M.;
 RT "Sequence and expression of mRNAs encoding the alpha 1 and alpha 2
 RT subunits of a DHP-sensitive calcium channel.";
 RL Science 241:1661-1664 (1988).
 [3] BETA-SUBUNIT BINDING DOMAIN
 MEDLINE=94150724; PubMed=7509046;
 RA Praetzel M., de Waard M., Mori Y., Tanabe T., Snutch T.P.,
 RA Campbell K.P.;
 RT "Calcium channel beta-subunit binds to a conserved motif in the I-II
 RT cytoplasmic linker of the alpha 1-subunit.";
 RL Nature 368:67-70 (1994).
 [4] PHENYLALKYLAMINE-BINDING SITE
 MEDLINE=91067656; PubMed=2174553;
 RA Striebing J., Grossmann H., Catterall W.A.;
 RT "Identification of a phenylalkylamine binding region within the alpha 1
 RT subunit of skeletal muscle Ca²⁺ channels.";

RL RN DIHYDROPYRIDINE-BINDING SITE.
 RP RX MEDLINE=2021019; PubMed=1656465;
 RA RA
 RA Kanaoka Y., Taki M., Striebing J., Grossmann H., Catterall W.A.,
 RT "Identification of 1,4-dihydropyridine binding regions within the alpha 1 subunit of skeletal muscle Ca²⁺ channels by photoaffinity labeling with diazapine.";
 RP RT proc. Natl. Acad. Sci. U.S.A. 88:9203-9207 (1991).
 [6] DIHYDROPYRIDINE-BINDING SITE
 RX MEDLINE=92073369; PubMed=1660150;
 RA Striebing J., Murphy B.J., Catterall W.A.;
 RT "Dihydropyridine receptor of L-type Ca²⁺ channels: identification of binding domains for [³H]azidopine within the alpha 1 subunit.";
 RP RT Proc. Natl. Acad. Sci. U.S.A. 88:10769-10773 (1991).
 [7] PHOSPHORYLATION OF SER-687 AND SER-1617.
 RX MEDLINE=89008428; PubMed=2844809;
 RA Roehrkasten A., Meyer H.B., Nastainczyk W., Sieber M., Hofmann F.;
 RT "cAMP-dependent protein kinase rapidly phosphorylates serine-687 of the skeletal muscle receptor for calcium channel blockers.";
 RL RL J. Biol. Chem. 263:15325-15329 (1988).
 [8] RP PHOSPHORYLATION BY CAPK.
 RX MEDLINE=89367340; PubMed=2549550;
 RA Nuncio K., Florio V., Catterall W.A.;
 RT "Activation of purified calcium channels by stoichiometric protein phosphorylation.";
 RT PT Proc. Natl. Acad. Sci. U.S.A. 86:6816-6820 (1989).
 CC -1- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCCs) MEDIATE THE ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION, CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1S GIVES RISE TO L-TYPE CALCIUM CURRENTS. LONG-LASTING (L-TYPE) CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP. THEY ARE BLOCKED BY DIHYDROPYRIDINES (DHP), PHENYLALKYLAMINES, BENZOTHIAPIPINES, AND BY OMEGA-AGATOKIN-III (OMEGA-AGA-III). THEY ARE HOWEVER INSENSITIVE TO OMEGA-CONOTOXIN-GVIA (OMEGA-CTP-GVIA) AND OMEGA-AGATOKIN-IVA (OMEGA-AGA-IVA).
 CC CALCIUM CHANNELS CONTAINING THE ALPHA-1S SUBUNIT PLAY AN IMPORTANT ROLE IN EXCITATION-CONTRACTION COUPLING IN SKELETAL MUSCLE.
 CC -1- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA CC LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY. AN ADDITIONAL GAMMA SUBUNIT IS PRESENT ONLY IN SKELETAL MUSCLE L-TYPE CHANNEL.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: SKELETAL MUSCLE SPECIFIC.
 CC -1- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
 CC -1- DOMAIN: THE LOOP BETWEEN REPEATS II AND III INTERACTS WITH THE RYANODINE RECEPTOR, AND IS THEREFORE IMPORTANT FOR CALCIUM RELEASE FROM THE ENDOPLASMIC RETICULUM, NECESSARY FOR MUSCLE CONTRACTION.
 CC -1- PTM: THE ALPHA-1S SUBUNIT IS FOUND IN TWO ISOFORMS IN THE SKELETAL MUSCLE: A MINOR FORM OF 212 kDa CONTAINING THE COMPLETE AMINO ACID SEQUENCE, AND A MAJOR FORM OF 190 kDa DERIVED FROM THE FULL-LENGTH FORM BY POST-TRANSLATIONAL PROTEOLYSIS CLOSE TO PHE-1690.
 CC -1- PTM: BOTH THE MINOR AND MAJOR FORMS ARE PHOSPHORYLATED IN VITRO BY CAPK. PHOSPHORYLATION BY CAPK STIMULATES THE CALCIUM CHANNEL.
 CC -1- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS FAMILY.

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 CC

DR EMBL; X05921; CAA29355.1; - .
 DR BMBL; M23919; AAA31159.1; - .
 DR PIR; A30053; A30063; .
 DR PDB; 1DU1; 19-JUL-00; .
 DR InterPro; IPR001682; Ca/Na_pore.
 DR InterPro; IPR002111; Ca²⁺ channel_TrpL.
 DR InterPro; IPR0052077; Ca channel.
 DR InterPro; IPR005446; LVDCCA_Alpha1.
 DR InterPro; IPR005450; LVDCCA_Alpha1S.
 DR InterPro; IPR005820; M+channel_nlg.
 DR Pfam; PF00520; ion_trans_4.
 DR PRINTS; PR00167; C4CHANNEL.
 DR PRINTS; PR01630; LVDCCALPHA1.
 DR PRINTS; PR01634; LVDCCALPHA1S.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Calcium channel; Glycoprotein; Repeat; Multigene family;
 KW Calcium-binding; Phosphorylation; Polymorphism; 3D-structure.
 PT REPEAT 38 337 I.
 PT REPEAT 418 664 III.
 PT REPEAT 786 1068 III.
 PT REPEAT 1105 1384 IV.
 PT DOMAIN 1 51 CYTOPLASMIC (POTENTIAL).
 PT TRANSMEM 52 70 S1 OF REPEAT I (POTENTIAL).
 PT DOMAIN 71 88 EXTRACELLULAR (POTENTIAL).
 PT TRANSMEM 89 108 S2 OF REPEAT I (POTENTIAL).
 PT DOMAIN 109 120 CYTOPLASMIC (POTENTIAL).
 PT TRANSMEM 121 139 S3 OF REPEAT I (POTENTIAL).
 PT DOMAIN 140 160 EXTRACELLULAR (POTENTIAL).
 PT TRANSMEM 161 179 S4 OF REPEAT I (POTENTIAL).
 PT DOMAIN 180 198 CYTOPLASMIC (POTENTIAL).
 PT TRANSMEM 199 218 S5 OF REPEAT I (POTENTIAL).
 PT DOMAIN 219 309 EXTRACELLULAR (POTENTIAL).
 PT TRANSMEM 310 334 S6 OF REPEAT I (POTENTIAL).
 PT DOMAIN 335 432 CYTOPLASMIC (POTENTIAL).
 PT TRANSMEM 433 451 S1 OF REPEAT II (POTENTIAL).
 PT DOMAIN 452 466 EXTRACELLULAR (POTENTIAL).
 PT TRANSMEM 467 486 S2 OF REPEAT II (POTENTIAL).
 PT DOMAIN 487 494 CYTOPLASMIC (POTENTIAL).
 PT TRANSMEM 495 513 S3 OF REPEAT II (POTENTIAL).
 PT DOMAIN 514 523 EXTRACELLULAR (POTENTIAL).
 PT TRANSMEM 524 542 S4 OF REPEAT II (POTENTIAL).
 PT DOMAIN 543 561 CYTOPLASMIC (POTENTIAL).
 PT TRANSMEM 562 581 S5 OF REPEAT II (POTENTIAL).
 PT DOMAIN 582 636 EXTRACELLULAR (POTENTIAL).
 PT TRANSMEM 637 661 S6 OF REPEAT II (POTENTIAL).
 PT DOMAIN 662 799 S1 OF REPEAT III (POTENTIAL).
 PT TRANSMEM 800 818 EXTRACELLULAR (POTENTIAL).
 PT DOMAIN 819 834 S2 OF REPEAT III (POTENTIAL).
 PT TRANSMEM 835 854 EXTRACELLULAR (POTENTIAL).
 PT DOMAIN 855 866 CYTOPLASMIC (POTENTIAL).
 PT TRANSMEM 867 885 S3 OF REPEAT III (POTENTIAL).
 PT DOMAIN 886 892 EXTRACELLULAR (POTENTIAL).
 PT TRANSMEM 893 911 S4 OF REPEAT III (POTENTIAL).
 PT DOMAIN 912 930 CYTOPLASMIC (POTENTIAL).
 PT TRANSMEM 931 950 S5 OF REPEAT III (POTENTIAL).
 PT DOMAIN 951 1040 S2 OF REPEAT III (POTENTIAL).
 PT TRANSMEM 1041 1065 S6 OF REPEAT III (POTENTIAL).
 PT DOMAIN 1066 1118 CYTOPLASMIC (POTENTIAL).
 PT TRANSMEM 1119 1137 S3 OF REPEAT IV (POTENTIAL).
 PT DOMAIN 1138 1152 EXTRACELLULAR (POTENTIAL).
 PT TRANSMEM 1153 1172 S2 OF REPEAT IV (POTENTIAL).
 PT DOMAIN 1173 1180 CYTOPLASMIC (POTENTIAL).
 PT TRANSMEM 1181 1199 S3 OF REPEAT IV (POTENTIAL).

FT DOMAIN 1200 1231 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1232 1250 S4 OF REPEAT IV (POTENTIAL).
 FT DOMAIN 1251 1269 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1270 1289 S5 OF REPEAT IV (POTENTIAL).
 FT DOMAIN 1290 1356 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1357 1381 S6 OF REPEAT IV (POTENTIAL).
 FT DOMAIN 1382 1873 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 357 374 BINDING TO THE BETA SUBUNIT.
 FT DOMAIN 562 568 POLY LEU.

Query Match Score 95; DB 1; Length 1873;
 Best Local Similarity 24.0%; Pred. No. 1.8; Mismatches 31; Gaps 9;
 Matches 46; Conservative 31; Mi mismatches 69; Indels 46; Gaps 9;

Qy 12 SNSCCUCCHYRTGTLLGWYLINAVVILLSLRLA---DPDQYNSSELGGDFEFM 67
 Drb 785 TNKFRVLCH---RIVNATWF-TNFILLFILLSSAALAEDPRAESVNRQILQYFD-- 836
 Qy 68 DDANNNCIATAISLMLICAMATGAYKQRAAWIIPFFCYQIDFALNMVATVLIYPN 127
 Drb 837 -----IAFTSVFTVETRIVLRTTYGKLS---FCRNYYFN1-LDILVVAVSLI--- 881
 Qy 128 SIQETVRLDPNPPYRQDDVMSVNPTPCLVILLFISIITFKG-YLISCVWNVCYRYING 185
 Drb 882 -----SMGLESSTISVVKILRVLVRPRAINRAKGLKHVVQCVFVAIRTIGN 930
 Qy 186 RNSSPDVLYVTS 197
 Drb 931 -----IVLVTT 936

RESULT 6
 CCAS RATE STANDARD PRT 1146 AA.
 ID CCAS RATE ID PRT
 AC Q0285; P70484; Q01553; Q62817;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Voltage-dependent L-type calcium channel alpha-1S subunit (Calcium
 channel, L type, alpha-1 polypeptide, isoform 3, skeletal muscle)
 DE (ROB) (Fragment).
 DE (ROB) (Fragment).
 GN CACHN1 OR CAGNLIA3 OR CACN1 OR CACN1 OR CCL1A3.
 OS Rattus norvegicus (Rat).
 OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93122775; PubMed=13335956;
 RX Chin H., Krali M., Kim H.-L., Kozak C.A., Mock B.A.;
 RA "The gene for the alpha-1 subunit of the skeletal muscle
 RT dihydropyridine-sensitive calcium channel (CCh1a3). maps to mouse
 RT chromosome 1.";
 RL Genomics 14:1089-1091 (1992).
 RN [2]
 RP SEQUENCE OF 597-691 FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=93066365; PubMed=1276681;
 RA Yu A.S.L., Hebert S.C., Bremner B.M., Lytton J.;
 RA "Molecular characterization and nephron distribution of a family of
 RT transcripts encoding the pore-forming subunit of Ca²⁺ channels in the
 RT kidney.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:10494-10498 (1992).
 RN [3]
 RP SEQUENCE OF 359-658 FROM N.A. (ISOFORM ROB1).
 RC TISSUE=Osteosarcoma;
 RX MEDLINE=96074517; PubMed=747909;
 RA Bary E.L.R., Geseb P.A., Froehner S.C., Friedman P.A.;
 RA "Multiple calcium channel transcripts in rat osteosarcoma cells:
 RT selective activation of alpha 1D isoform by parathyroid hormone.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:10914-10918 (1995).
 RN [4]
 RP PHOSPHORYLATION BY CAPK.

SEQUENCE FROM N.A. PubMed=8920183;
 RX MEDLINE=91077616; PubMed=8920183;
 RA Dwivedi P.P., Gibbs M.D., Sauv D.J., Bergquist P.L.; Bergquist P.L.;
 RT "Cloning, sequencing and overexpression in *Escherichia coli* of a
 RT xylanase, xynA from the thermophilic bacterium *RtOB*.4 genus
 RT *Caldicellulobacter*.";
 RT Appl. Microbiol. Biotechnol. 45:86-93 (1996).
 CC 1-- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC 1-- SIMILARITY: BELONGS TO THE BINDING-PROTEIN-DEPENDENT TRANSPORT
 CC SYSTEM PERMEASE FAMILY. MALFG SUBFAMILY.
 CC
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 DR EMBL; L18965; AAB42042.1;
 PIR; S41786; S41786.
 DR IN-PRO; IPR000515; BPD transport.
 DR Pfam: PF00528; BPD transport.
 DR PROSITE; PS00402; BPD-TRANS-MEMBR; 1.
 DR PROSITE; PS00402; BPD-TRANS-INN-MEMBR; 1.
 KW Hypothetical protein; Transmembrane; Transport.
 FT TRANSMEM 11 31 POTENTIAL.
 FT TRANSMEM 74 94 POTENTIAL.
 FT TRANSMEM 108 128 POTENTIAL.
 FT TRANSMEM 136 156 POTENTIAL.
 FT TRANSMEM 185 205 POTENTIAL.
 FT TRANSMEM 239 259 POTENTIAL.
 SQ SEQUENCE 275 AA; 30857 MW; BDT7A3246B4F50199 CRC64;
 DR
 Query Match 7.7%; Score 92.5%; DB 1; Length 275;
 Best Local Similarity 22.3%; Pred. No. 0.44%;
 Matches 53; Conservative 33; Mismatches 69; Indels 83; Gaps 9;
 DR
 Qy 26 ILLGVVYLINAVVLLILSAL-----ADPQQYNSSSSELGDDPFEMDDA 70
 Db 13 IFLAVWTIADVPFLMLFTSFKTQSELSGNTWQLPQQPTIGNFSTVLEGNNFTYL-K 70
 DR
 Qy 71 NCIAIAISISSLML-TCAIATGYAKQRAAWIIPPFYCQYDFALN-----MLVA 119
 Db 71 NSVIAVSISSVLLIISMPA-----PAPSRPKFALNNLILYSLIAGMAIP 116
 DR
 Qy 120 ITVLTP-----NSIO-----EYTRQLPNPFYRQDVMV 149
 Db 117 IHVTLPIVYLTNKTLYDVTYFALIGPYVALSLPMSIFLTGMRPIPLBEAKIDGC 176
 DR
 Qy 150 NPTCLVILILFIS--IILTFKGYLISCVNNCYRYINGRNSDVYTTNTVILP 205
 DR :-----:-----:-----:-----:-----:-----:-----:-----:
 DE NADH-ubiquinone oxidoreductase chain 1 (EC 1.6.5.3).
 GN NDI OR NADH1.
 OS Trichophyton rubrum.
 OG Mitochondrion.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Onygenales; Archamycotae; mitosporic Archamycotae;
 OC Trichophyton.
 OC NCBI_TaxID=5551;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IP 1817-89;
 RX MEDLINE=9146870; PubMed=10022946;

RA de Bievre C., Dujon B.; genome of *Trichophyton rubrum* III.
 RT "Organisation of the mitochondrial genome of the NADH dehydrogenase subunits 1, 2, 3, 4,
 RT 5 and the cytochrome b gene.";
 RT Curr. Genet. 35:30-35 (1999).
 RL -|- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
 CC -|- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 1 FAMILY.
 CC
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 CC
 DR EMBL; Y18476; CAA77189.1; -.
 PIR; T14245; T14245.
 DR InterPro; IPR001694; ResP_NADH_dh1.
 DR Pfam: PF00146; NADidh; 1.
 DR PROSITE; PS00667; COMPLEX1_ND1-1; 1.
 DR PROSITE; PS00668; COMPLEX1_ND1-2; 1.
 KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transmembrane.
 SQ SEQBNCE 343 AA; 38239 MW; D29CD3BF97CFBD64 CRC64;
 DR
 Query Match 7.6%; Score 91; DB 1; Length 343;
 Best Local Similarity 21.7%; Pred. No. 0.74%;
 Matches 47; Conservative 45; Mismatches 67; Indels 58; Gaps 12;
 DR
 Qy 9 RFYNSNSCCCLCHVRYGTILLG-----WYLI-INAVALLILLISALLADPDQYNSSE 59
 DR 153 RFY----ILVILVFTGSLNLNTTIESQKVVYFILELLPFLIFFGCGIAETNRAFPDLAE 208
 DR
 DR 60 LGGDP----EMDDANCMIAISL-----MILICMAMT---YGAJKQRAAWIIPFCYQI 109
 DR 209 AESELVSGMTEHSAVIENTIFFLQAYASIVLICLSSYLFLGGYLN----ILPNTNYV 264
 DR
 DR 110 FDF----ALMMLVAVTLLVYPSNQYIRQLPPNPFYRQDVMVSNFTCLVL 156
 DR 265 CDFNSLFSDSLNGISSLNLAIKPLFLF--VPLVWRAFSPTRIF-DQLMMSVCTVILLP 320
 DR
 DR 157 ILLLISIILTFKGYLISCVNNCYRYINGRNSDVYTTNTVILP 193
 DR 321 IIIAVY----VLLPCTI----VIGLNSSILLI 343
 DR
 DR AAP-2 OR AAP2.
 DR
 DR 9
 DR AAP2_NEURC
 DR ID AAP2_NEURC STANDARD; PRT; 551 AA.
 DR AC 059472;
 DR DT 15-DEC-1998 (Rel. 37, Created)
 DR DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DR DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DR DB Amino acid permease 2.
 DR
 DR GN Neurospora crassa.
 DR OC Sorcaria; Sorcaria; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 DR OC Sorcariaceae; Sorcariales; Sordariaceae; Neurospora.
 DR OC NCBI_TaxID=5111;
 DR RN [1]
 DR SEQUENCE FROM N.A.
 DR RA Marpolles Clark E., Bowman B.J.; GenBank/GenBank/DBJ databases.
 DR RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 DR CC -|- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
 DR CC -|- SIMILARITY: Belongs to the amino acid permease family.
 DR
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 DR

CC	EMBL; AAC0355.1;	Montmayeur J.-P.; Matsunami H.;	Receptors for bitter and sweet taste.;
DR	InterPro; IPR002293; AA_irel;	Curr. Opin. Neurobiol.	12:366-371 (2002).
DR	InterPro; IPR004756; AA_permease.	[4]	
DR	InterPro; IPR004840; AAC_permease.	REVIEW.	
DR	InterPro; IPR004841; Permease.	MEDLINE=21634924; PubMed=11696554;	
DR	Pfam; PF00324; aa_Permeases;	RX	
DR	TIGR0907; TIGR0908;	RA	
DR	PROSITE; PS00218; AMINO_ACID_PERMEASE_1;	RA	"Molecular mechanisms of bitter and sweet taste transduction.;"
KW	Transport; Amino-acid transport; Transmembrane.	RT	
FT	TRANSMEM 66 86	RL	J. Biol. Chem. 277:1-4 (2002).
FT	TRANSMEM 90 110	RN	[5]
FT	TRANSMEM 139 159	RP	REVIEW.
FT	TRANSMEM 188 208	RX	MEDLINE=22469025; PubMed=12581520;
FT	TRANSMEM 214 234	RA	Zhang Y.-Hoon M.A.; Chandrashekar J.; Mueller K.L.; Cook B.; Wu D.; Zuker C.S.; Ryba N.J.;
FT	TRANSMEM 255 275	RA	"Coding of sweet, bitter, and umami tastes: different receptor cells sharing similar signaling pathways.;"
FT	TRANSMEM 301 321	RT	RT
FT	TRANSMEM 347 367	RL	Cell 112:293-301 (2003).
FT	TRANSMEM 399 419	CC	-I- FUNCTION: Receptor that may play a role in the perception of bitterness and is gustducin-linked. Activated by denatonium and 6-n-propyl-2-thiouracil. May play a role in sensing the chemical composition of the gastrointestinal content. The activity of this receptor may stimulate alpha gustducin, mediate PLC-beta-2 activation and lead to the gating of TRPM5.
FT	TRANSMEM 424 444	CC	-I- SUBCELLULAR LOCATION: Integral membrane protein.
FT	TRANSMEM 464 484	CC	-I- TISSUE SPECIFICITY: Expressed in subsets of taste receptor cells of the tongue and palate epithelium and exclusively in gustducin-positive cells. Expressed in 15% taste bud cells in circumvallate and foliate papillae but only in 2% in fungiform papillae.
FT	TRANSMEM 496 516	CC	-I- MISCELLANEOUS: Most taste cells may be activated by a limited number of bitter compounds; individual taste cells can discriminate among bitter stimuli.
SQ	SEQUENCE 551 AA; 59869 MW; CB12C646B82F9ADF CRC64;	CC	-I- SIMILARITY: Belongs to family T2R of G-protein coupled receptors. CAUTION: This protein was previously referred to T2R8, but due to its high similarity towards the human T2R4 sequence it is considered to be T2R4.
CC		CC	
CC		CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation of the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC		CC	
CC		CC	DR
CC		CC	Pfam; PF05296; TAS2R; 1.
CC		CC	Receptor; G-protein coupled receptor; Transmembrane.
CC		CC	EXTRACELLULAR (POTENTIAL).
CC		CC	DOMAIN 1 11
CC		CC	FT TRANSMEM 1 12
CC		CC	FT DOMAIN 3 32
CC		CC	FT TRANSMEM 3 46
CC		CC	FT DOMAIN 4 67
CC		CC	FT TRANSMEM 6 68
CC		CC	FT DOMAIN 8 80
CC		CC	FT TRANSMEM 8 101
CC		CC	FT DOMAIN 10 128
CC		CC	FT TRANSMEM 12 149
CC		CC	FT DOMAIN 15 171
CC		CC	FT TRANSMEM 17 192
CC		CC	FT DOMAIN 19 229
CC		CC	FT TRANSMEM 23 250
CC		CC	FT DOMAIN 25 260
CC		CC	FT TRANSMEM 26 281
CC		CC	FT DOMAIN 28 297
CC		CC	FT CARBOHYD 163 163
CC		CC	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE 297 AA; 34202 MW; EC2C1EAE06571F80 CRC64;	CC	
Query Match	7.4%; Score 89; DB 1; Length 297;		
Best Local Similarity	24.7%; Pred. No. 0.96; Gaps 9;		
Matches	48; Conservative 30; Mismatches 76; Indexes 40;		
Qy	21 VRTGILLGWYLNAVLLILAS		
Db	9 VFAASVFLNFGVITANLFIIVIKTWNNSRRIASPDRILF-----L 51		

Y	75	AIASISLMLICAMPTYGAYKQ-RPAW11PPF--CYQIPDPALNNLVAVTFL--IYPNSI	129
Y	52	AITRFITLGIPLASVSVIATNTGGSVYFSTFLCKWFLD-ANSILWLTILNSIVCVKI	109
Y	130	QEYIRQLPPLNPYRQDVMNSYPTCQLVLTIFLISITLTFKGYLYSICWVNCYRINGRN-	187
Y	110	TNFQH--PVFLILKRTISMKTTSLLACHL-ISALTLIYMSQISRPFPEHIGRNDT	165
Y	188	---	SDVLYVYTS 197
Y	166	SFDLSGDLTFLVAS	179
RESULT 11.			
		CCAD-ME5AU	STANDARD
		Q92244; Q99245;	PRT
		15-JUL-1999 (Rel. 38, Created)	
		15-JUL-1999 (Rel. 38, Last sequence update)	
		15-SEP-2003 (Rel. 42, Last annotation update)	
		Voltage-dependent L-type calcium channel alpha-1D subunit (Calcium	
		channel, L type, alpha-1, polypeptide isoform 2).	
		CaNCR1 OR CACN1A2 OR CCHL2A2 OR CACN3 OR CACN4.	
		Mesocricetus auratus (Golden hamster).	
		Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
		Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;	
		Mesocricetus	
		NCBI_TaxID=10336;	
	[1]	SEQUENCE FROM N.A. (ISOFORM HCA3A).	
		SEQUENCE=Insulinoma;	
		MEDLINE=93149124; PubMed=1337146;	
		Perez-Reyes E., Wheeler M.B., Wei X., Birnbaumer L.,	
		Yaneff G.C., Wheeler M.B., Wei X., Perez-Reyes E., Birnbaumer L.,	
		Boyd A.E. III, Moss L.G.;	
		"Cloning of a novel alpha 1-subunit of the voltage-dependent calcium	
		channel from the beta-cell,"	
		Mol. Endocrinol. 6:2143-2152 (1992).	
	[2]	SEQUENCE OF 1146-1441 FROM N.A. (ISOFORMS CACN3B AND CACN3D).	
		TISSUE=Heart;	
		MEDLINE=1056091; PubMed=2173707;	
		Perez-Reyes E., Wei X., Birnbaumer L., Birnbaumer A.,	
		"Molecular diversity of L-type calcium channels. Evidence for	
		alternative splicing of the transcripts of three non-allelic genes."	
		J. Biol. Chem. 265:10430-10436 (1990).	
		-1- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE	
		ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED	
		IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE	
		CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,	
		CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1D	
		CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (L-TYPE)	
		GROUP. THEY ARE BLOCKED BY DIHYDROPYRIDINES (DHP),	
		PHENYLALKYLAMINES, BENZOTHIAZIPILES, AND BY OMEGA-AGATOKIN-IIIa	
		(OMEGA-AGA-IIIa). THEY ARE, HOWEVER, INSENSITIVE TO OMEGA-CONTOXIN-	
		GVIA (OMEGA-CPX-GVIA) AND OMEGA-AGATOKIN-IVA (OMEGA-AGA-IVA).	
		-1- SUBUNIT: VOLTAGE DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT	
		COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS	
		IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-	
		FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS	
		SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM	
		CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA	
		LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.	
	-1-	ALTERNATIVE PRODUCTION:	
	-1-	Event=Alternative splicing; Named isoforms=3;	
		Comment=Additional isoforms seem to exist;	
		Name=HCA3B;	
		IsID=Q92244-1; Sequence=Displayed;	
		Name=CACN3B;	
		IsID=Q99244-3; Sequence=Not described;	
		Name=CACN3D;	
		IsID=Q99244-2; Sequence=VSP 000915;	
		Name=CACN3E;	

RESULT 12

CCAD_HUMAN	STANDARD	PRT;	2161 AA.
AC	Q01668; Q13916; Q11931;		
DT	15-JUL-1999 (Rel. 38, Created)		
DT	15-JUL-1999 (Rel. 38, Last sequence update)		
DT	15-SEP-2003 (Rel. 42, Last annotation update)		
DE	Voltage-gated L-type calcium channel alpha-1 subunit (Calcium channel, L type, alpha-1 polypeptide, isoform 2).		
GN	CACNA1D OR CACNL1A2 OR CACH3 OR CACN4.		
OS	Homo sapiens (Human).		

Query Match 7.4%; Score 88.5%; DB 1; Length 1610;

Best Local Similarity 25.0%; Pred. No. 5.7;

Matches 46; Conservative 34; Mismatches 61; Indels 43; Gaps 10;

Qy 21 VRTGTLGWLGYWLLINAVVLLILSALA---DP-DQYNPSSSEIG-GFEEFMDDANMCI 74

Db 873 IRVGCHKLINHFIITNLIVLIMLSSAALAAEDPFRSHSPRTNLYGFYDFP----- 924

Qy 75 AIAISLIMLICAMATYGAKEYKQRAWIIIPPFYCQIFDFAALMVLVITVLIYPNSIQEYR 134

Db 925 -TAIFVELL-KMTTGFAGFLHKG-----FCRAYFNL-LDMLVYGVSVL----- 966

Qy 135 QLPPNPYRDVMSVNPFLVLLFLFISLTLFKG--VLIJSCWNCVYRINGRNSSDVL 192

Db 967 ---SFGIQSSAISVYKILVRLVRPLRAINRAGLKHVQCYFAIRTI---GNIM 1017

Qy 193 VVVT 196

Db 1018 IVTT 1021

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. NCBI TaxID=9606;

OX [1]

RN RP SEQUENCE FROM N.A. (ISOFORM NEURONAL-TYPE).

RC TISSUE=Neuroblastoma; MEDLINE=92110010; PubMed=1309651;

RX RA Williams M.E., Feldman D.H., McCue A.F., Brenner R., Velicelebi G., Ellis S.B., Harpold M.N.; "Structure and functional expression of alpha 1, alpha 2, and beta subunits of a novel human neuronal calcium channel subtype." [2]

RN RP SEQUENCE FROM N.A. (ISOFORM BETA-CELL-TYPE).

RC TISSUE=Pancreatic islets; MEDLINE=92115705; PubMed=1309948;

RX Seino S., Chen L., Seino M., Blondel O., Takeda J., Johnson J.H., Bell G.I.; "Cloning of the alpha 1 subunit of a voltage-dependent calcium channel expressed in pancreatic beta cells." [3]

RN RP SEQUENCE FROM N.A. (ISOFORM BETA-CELL-TYPE), AND VARIANT NIDDM. MEDLINE=96044438; PubMed=7557998;

RX RA Yamada Y., Masuda K., Li Q., Tharay Y., Kubota A., Miura T., Nakamura K., Fujii Y., Seino Y.; "The structures of the human calcium channel alpha 1 subunit (CACNL1A2) and beta subunit (CACNLB3) genes." [4]

RN RP FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCCs) MEDIATE THE ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1 Dihydropyridines (DHP) GIVES RISE TO LTYPE CALCIUM CURRENTS. LONG-LASTING (L-TYPE) CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP. THEY ARE BLOCKED BY DIHYDROPYRIDINES (DHP), (OMEGA-AGA-IIIA), BENZODIAPINES, AND BY OMEGA-AGA-TOXIN-111A (OMEGA-AGA-IIIA). THEY ARE HOWEVER INSENSITIVE TO OMEGA-CONOTOXIN-GVIA (OMEGA-GVIA) AND OMEGA-AGA-TOXIN-11A (OMEGA-AGA-IVA).

RL Genomics 27:312-319 (1995).

CC -I- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE ALPHA-1 SUBUNIT. IN MANY CASES, THIS SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.

CC -I- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=2; Comment=Additional isoforms seem to exist;

CC Name=Neuronal-type; IsoId=Q01668-1; Sequence=Displayed;

CC Name=Beta-cell-type; IsoId=Q01668-2; Sequence=YSP 000914;

CC -I- TISSUE SPECIFICITY: EXPRESSED IN PANCREATIC ISLETS AND IN BRAIN, WHERE IT HAS BEEN SEEN IN HIPPOCAMPUS, BASAL GANGLIA, HABENULA AND THALAMUS. NO EXPRESSION IN SKELETAL MUSCLE.

CC -I- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS ARE PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.

CC -I- POLYMORPHISM: A CHANGE FROM SEVEN TO EIGHT ATG TRINUCLEOTIDE REPEATS, RESULTING IN AN ADDITIONAL N-TERMINAL METHIONINE, HAS BEEN FOUND IN A PATIENT WITH NON-INSULIN-DEPENDENT DIABETES MELLITUS (NIDDM).

CC -I- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS FAMILY.

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CC	EMBL; M76580; AAAS5629.1; -;	FT DOMAIN	1192	1467
CC	EMBL; M83566; AAA35629.1; -;	FT TRANSMEM	121	126
CC	EMBL; D43747; BRA07804.1; JOINED.	FT DOMAIN	127	145
CC	EMBL; D43705; BRA07804.1; JOINED.	FT TRANSMEM	146	163
CC	EMBL; D43706; BRA07804.1; JOINED.	FT DOMAIN	164	183
DR	EMBL; D43707; BRA07804.1; JOINED.	FT TRANSMEM	184	195
DR	EMBL; D43708; BRA07804.1; JOINED.	FT DOMAIN	196	214
DR	EMBL; D43709; BRA07804.1; JOINED.	FT TRANSMEM	215	235
DR	EMBL; D43710; BRA07804.1; JOINED.	FT DOMAIN	235	254
DR	EMBL; D43711; BRA07804.1; JOINED.	FT TRANSMEM	254	273
DR	EMBL; D43712; BRA07804.1; JOINED.	FT DOMAIN	274	293
DR	EMBL; D43713; BRA07804.1; JOINED.	FT TRANSMEM	294	381
DR	EMBL; D43714; BRA07804.1; JOINED.	FT DOMAIN	382	406
DR	EMBL; D43715; BRA07804.1; JOINED.	FT TRANSMEM	407	523
DR	EMBL; D43716; BRA07804.1; JOINED.	FT DOMAIN	605	614
DR	EMBL; D43717; BRA07804.1; JOINED.	FT TRANSMEM	615	633
DR	EMBL; D43718; BRA07804.1; JOINED.	FT DOMAIN	634	652
DR	EMBL; D43719; BRA07804.1; JOINED.	FT TRANSMEM	653	673
DR	EMBL; D43720; BRA07804.1; JOINED.	FT DOMAIN	674	727
DR	EMBL; D43721; BRA07804.1; JOINED.	FT TRANSMEM	728	752
DR	EMBL; D43722; BRA07804.1; JOINED.	FT DOMAIN	753	886
DR	EMBL; D43723; BRA07804.1; JOINED.	FT TRANSMEM	887	905
DR	EMBL; D43724; BRA07804.1; JOINED.	FT DOMAIN	906	921
DR	EMBL; D43725; BRA07804.1; JOINED.	FT TRANSMEM	922	941
DR	EMBL; D43726; BRA07804.1; JOINED.	FT DOMAIN	942	953
DR	EMBL; D43727; BRA07804.1; JOINED.	FT TRANSMEM	954	972
DR	EMBL; D43728; BRA07804.1; JOINED.	FT DOMAIN	973	978
DR	EMBL; D43729; BRA07804.1; JOINED.	FT TRANSMEM	979	998
DR	EMBL; D43730; BRA07804.1; JOINED.	FT DOMAIN	999	1017
DR	EMBL; D43731; BRA07804.1; JOINED.	FT TRANSMEM	1018	1037
DR	EMBL; D43732; BRA07804.1; JOINED.	FT DOMAIN	1038	1127
DR	EMBL; D43733; BRA07804.1; JOINED.	FT TRANSMEM	1128	1148
DR	EMBL; D43734; BRA07804.1; JOINED.	FT DOMAIN	1149	1205
DR	EMBL; D43735; BRA07804.1; JOINED.	FT TRANSMEM	1206	1224
DR	EMBL; D43736; BRA07804.1; JOINED.	FT DOMAIN	1225	1239
DR	EMBL; D43737; BRA07804.1; JOINED.	FT TRANSMEM	1240	1259
DR	EMBL; D43738; BRA07804.1; JOINED.	FT DOMAIN	1260	1266
DR	EMBL; D43739; BRA07804.1; JOINED.	FT TRANSMEM	1267	1288
DR	EMBL; D43740; BRA07804.1; JOINED.	FT DOMAIN	1289	1313
DR	EMBL; D43741; BRA07804.1; JOINED.	FT TRANSMEM	1314	1333
DR	EMBL; D43742; BRA07804.1; JOINED.	DR	Query Match	7.4%
DR	EMBL; D43743; BRA07804.1; JOINED.	DR	Best Local Similarity	Score 88.5;
DR	EMBL; D43744; BRA07804.1; JOINED.	DR	Matches 46;	Pred. No. 7.6;
DR	EMBL; D43745; BRA07804.1; JOINED.	DR	Conservative 34;	Mismatches 61;
DR	EMBL; D43746; BRA07804.1; JOINED.	DR	Gaps 10;	Indels 43;
DR	Genew; HGNC:1394; CACNA1D.	DR		
DR	MIM: 114206; -;	DR		
DR	GO; GO:0005891; C: voltage-gated calcium channel complex; TAS.	Db		
DR	GO; GO:0015270; F:dihydropyridine-sensitive calcium channel a. . . ; TAS.	Db		
DR	GO; GO:0006832; P: small molecule transport; TAS.	Qy		
DR	InterPro; IPR001682; C/Na_pore.	Qy	75	AIATISLMLICAM/TYGKQRAWIIPPFYCQDFALNMLYATVLYPNS1QEVIR 134
DR	InterPro; IPR002177; Ca_channel_TrpL.	Db		
DR	InterPro; IPR002111; Ca ²⁺ channel_TrpL.	Db	927	-TAITPVEIL-KMTFGAFPLHKGK-----FCRNFNLF-LDMLYVGVSIL-----968
DR	InterPro; IPR005821; Ion_trans.	Qy		
DR	InterPro; IPR005446; LVDCCALpha1.	Db	135	QLPPHPPYRDDMSUNPTCLVILFISILTFKG-YLISCVWCYRNGRNSDVL 192
DR	InterPro; IPR005452; LVDCCALpha1D.	Db	969	-----SGIQSSAISVKKLRLVRPLRAINRAGLKHIVQCVFAVITI-----GNIM 1019
DR	InterPro; IPR005820; M+channel_nlq.	Qy		
DR	Pfam; PF00520; ion_trans_4.	Db	193	VVVT 196
DR	PRINTS; PRO0167; CACNA1D.	Db		
DR	PRINTS; PRO1630; LVDCCALpha1.	Db		
DR	Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;			
KW	Calcium channel; Glycoprotein; Repat; Multigene family; Polymorphism;			
KW	Calcium-binding; Phosphorylation; Alternative splicing; Polymorphism;			
KW	Triplet repeat expansion.			
FT	REPEAT 113 409			
FT	REPEAT 509 755			
FT	REPEAT 873 1155			
			RESULT 13	
			CCAD RAT	
			ID CCAD RAT	
			PRT 2203 AA	
			ID P27752; 009023; 009024; Q61542; Q62691; Q63491;	
			AC Q63492;	
			AC 01-OCT-1996 (Rel. 34, Created)	

DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Voltage-dependent L-type calcium channel alpha-1D subunit (calcium
 DE channel, L type, alpha-1 polypeptide, isoform 2) (RAT brain class D)
 DE (RBD).
 DE CACNA1D OR CACNL1A2 OR CCH1A2 OR CACN3 OR CACN4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10112.
 RN
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Inulinoma;
 RX MEDLINE=95280950; PubMed=7760845;
 RA Thara Y., Yamada Y., Fujii Y., Gono T., Yano H., Yasuda K.,
 RA Inagaki N., Seino S., Seino S.;
 RT "Molecular diversity and functional characterization of voltage-
 dependent calcium channels (CACN4) expressed in pancreatic beta-
 cells.";
 RT Mol. Endocrinol. 9:121-130 (1995).
 RL [12].
 RN
 RP SEQUENCE FROM N.A. (ISOFORMS 3; 6; 7; 8 AND 14).
 RC TISSUE=Brain;
 RX MEDLINE=91299328; PubMed=1648940;
 RA Hui A., Ellinor P.T., Kripanow O., Wang J.-J., Diebold R.J.,
 RA Schwartz A.;
 RT "Molecular cloning of multiple subtypes of a novel rat brain isoform
 of the alpha-1 subunit of the voltage-dependent calcium channel.";
 RL Neuron 7:35-44 (1991).
 RN
 RP SEQUENCE OF 1-125 FROM N.A.
 RX MEDLINE=96040125; PubMed=5533731;
 RA Kamp T.J., Mitas M., Fields K.L., Asoh S., Chin H., Marban E.,
 RA Nierenberg M.;
 RT "Transcriptional regulation of the neuronal L-type calcium channel
 alpha 1D subunit gene.";
 RT Cell. Mol. Neurobiol. 15:307-326 (1995).
 RL [4].
 RN
 RP SEQUENCE OF 1100-1410 FROM N.A. (ISOFORMS 11 AND 12).
 RC TISSUE=Kidney;
 RX MEDLINE=93066265; PubMed=1279581;
 RA Yu A.S.L., Hebert S.C., Brenner B.M., Lytton J.;
 RT "Molecular characterization and nephron distribution of a family of
 transcripts encoding the pore-forming subunit of Ca2+ channels in the
 kidney.";
 RT Proc. Natl. Acad. Sci. U.S.A. 89:10494-10498 (1992).
 RL [5].
 RN
 RP SEQUENCE OF 1218-1498 FROM N.A. (ISOFORM 13).
 RC TISSUE=Osteosarcoma;
 RX MEDLINE=96074617; PubMed=7479909;
 RA Barrig E.L.R., Geesek F.A., Froehner S.C., Friedman P.A.;
 RT "Multiple calcium channel transcripts in rat osteosarcoma cells:
 selective activation of alpha 1D isoform by parathyroid hormone.";
 RT Proc. Natl. Acad. Sci. U.S.A. 92:10914-10918 (1995).
 RL [6].
 RN
 RP SEQUENCE OF 1200-1493 FROM N.A. (ISOFORMS 3; 4; 5; 9 AND 10).
 RX MEDLINE=977276179; PubMed=9232351;
 RA Brereton H.M., Harland M.L., Froscio M., Petronijevic T.,
 RA Barrig E.J.;
 RT "Novel variants of voltage-operated calcium channel alpha-1 subunit
 transcripts in a rat liver-derived cell line: deletion in the IVS4
 voltage sensing region.";
 RT Proc. Natl. Acad. Sci. U.S.A. 92:3945-3950 (1995).
 RL [7].
 RN
 RP SEQUENCE OF 1307-1479 FROM N.A. (ISOFORM 3).
 RX MEDLINE=90239020; PubMed=1692234;
 RA Snutch T.P., Leonard J.P., Gilbert M.M., Lester H.A., Davidson N.;
 RT "Novel variants of a heterogeneous family of calcium channels";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:3391-3395 (1990).
 CC -1- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE
 CC ENTRY OF CALCIUM-DEPENDENT PROCESSES. INCLUDING MUSCLE
 CC IN A VARIETY OF EXCITABLE CELLS. AND ARE ALSO INVOLVED

CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION, CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1D GIVES RISE TO L-TYPE CALCIUM CURRENTS. LONG-LASTING (L-TYPE) CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP. THEY ARE BLOCKED BY DIHYDROPYRIDINES (DHP), PHENYLALKYLAMINES, BENZOTIAZEPINES, AND BY OMEGA-AGATOXIN-11IA (OMEGA-AGA-11IA). THEY ARE HOWEVER INSENSITIVE TO OMEGA-CONOTOXIN-GVIA (OMEGA-CTX-GVIA) AND OMEGA-AGATOXIN-1IVA (OMEGA-AGA-1IVA).

-1- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.

-1- SUBCELLULAR LOCATION: Integral membrane protein.

-1- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=14; Comment=The region sequenced in isoforms ROB3 and RKC5 is identical to CACN4;

Name=1; Synonyms=CACN4A;

IsoId=P27732-1; Sequence=Displayed;

Name=2; Synonyms=CACNAB;

IsoId=P27732-2; Sequence=VSP_000924;

Name=3; Synonyms=CACNA2A; Sequence=VSP_000923; RBD-55;

IsoId=P27732-3; Sequence=VSP_000921;

Name=4; Synonyms=Delta-IV-S3; Sequence=VSP_000920;

IsoId=P27732-4; Sequence=VSP_000919;

Name=5; Synonyms=Delta-IV-S4; Sequence=VSP_000918;

IsoId=P27732-5; Sequence=VSP_000922;

IsoId=P27732-6; Sequence=VSP_000920, VSP_000921;

Name=6; Synonyms=RB9;

IsoId=P27732-7; Sequence=VSP_000917;

Name=7; Synonyms=RB11;

IsoId=P27732-8; Sequence=VSP_000916;

Name=8; Synonyms=RB34;

IsoId=P27732-9; Sequence=VSP_000916;

Name=9; Synonyms=RH1;

IsoId=P27732-10; Sequence=VSP_000919;

Name=10; Synonyms=RH2;

IsoId=P27732-11; Sequence=VSP_000919;

Name=11; Synonyms=RKC5;

IsoId=P27732-13; Sequence=Not described;

Name=12; Synonyms=RKC6;

IsoId=P27732-14; Sequence=VSP_000919;

Name=13; Synonyms=ROB3;

IsoId=P27732-14; Sequence=Not described;

Name=14; Synonyms=Truncated;

IsoId=P27732-12; Sequence=VSP_000925, VSP_000926;

-1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, PANCREATIC ISLETS AND B-LYMPHOCYTES.

-1- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.

-1- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS FAMILY.

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DR D38101; BAA07282; 1; -

DR D38101; BAA07283; 1; -

DR M57682; AAA42015; 1; -

DR U14005; AAB60315; 1; -

DR M99221; AAA40895; 1; -

DR U49126; AAB61634; 1; -

DR U49126; AAB61635; 1; -

DR	EMBL; U49127; AAB61635.1; -.	NU2M_DROMA	STANDARD;	PRT;	274 AA.
DR	AAB61636.1; -.	ID NU2M_DROMA			
DR	InterPro; IPR001682; Ca_Na_pore.	AC P29167;			
DR	InterPro; IPR002077; Ca_channel.	DT 01-APR-1993 (Rel. 25, Created)			
DR	InterPro; IPR02111; Cat_channel_TrpL.	DT 01-APR-1993 (Rel. 25, Last sequence update)			
DR	InterPro; IPR005821; Ion_trans.	DT 15-APR-1999 (Rel. 38, Last annotation update)			
DR	InterPro; IPR03091; K_Channel.	DE NADH-ubiquinone oxidoreductase chain 2 (EC 1.6.5.3) (Fragment).			
DR	InterPro; IPR005446; LVDCCA1phal.	GN ND2			
DR	InterPro; IPR005452; LVDCCA1phal.	OS Drosophila mauritiana (Fruit fly).			
DR	InterPro; IPR005820; M-channel_nlg.	OG Mitochondrion.			
PFam	PF00220; Ion_trans; 4.	OG Eukaryote; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;			
DR	PRINTS; PR00167; CCHANNEL.	OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
DR	PRINTS; PR00169; KCHANNEL.	OC Ephydrioidea; Drosophilidae; Drosophila.			
DR	PRINTS; PR01630; LVDCCA1phal.	NCB_ TaxID=7226;			
DR	PRINTS; PR01636; LVDCCA1phal.	OX RN [1]			
KW	Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;	RP SEQUENCE FROM N.A.			
KW	Calcium channel; Glycoprotein; Repeat; Multigene family;	RP MEDLINE=1088857; PubMed=2124697;			
KW	Calcium-binding; Phosphorylation; Alternative splicing.	RX RA Satta Y.; Takahata N.;			
FT	REPEAT 112 408	RT "Evolution of Drosophila mitochondrial DNA and the history of the melanogaster subgroup."			
FT	REPEAT 528 774	RT Proc. Natl. Acad. Sci. U.S.A. 87:9558-9562 (1990).			
FT	REPEAT 892 1174	RL CATALYTIC ACTIVITY: NADH + ubi quinone = NAD(+)			
FT	REPEAT 1211 1486	CC + ubi quinol.			
FT	DOMAIN 1 126	CC -I- CATALYTIC ACTIVITY: NADH + ubi quinone = NAD(+)			
FT	TRANSEMM 127 145	CC -I- SUBCELLULAR LOCATION: Integral membrane protein.			
FT	DOMAIN 146 163	CC -I- Mitochondrial			
FT	TRANSEMM 164 183	CC -I- Melanogaster			
FT	DOMAIN 184 195	CC -I- Similarity: BELONGS TO THE COMPLEX I SUBUNIT 2 FAMILY.			
FT	TRANSEMM 196 214	CC This SWISS-PROT entry is copyright. It is produced through a collaboration			
FT	DOMAIN 215 235	CC between the Swiss Institute of Bioinformatics and the EMBL outstation -			
FT	TRANSEMM 236 254	CC the European Bioinformatics Institute. There are no restrictions on its			
FT	DOMAIN 255 273	CC use by non-profit institutions as long as its content is in no way			
FT	TRANSEMM 274 293	CC modified and this statement is not removed. Usage by and for commercial			
FT	DOMAIN 294 381	CC entities requires a license agreement (See http://www.isb-sib.ch/announce/			
FT	TRANSEMM 382 406	CC or send an email to licensee@isb-sib.ch).			
FT	DOMAIN 407 582	CC			
FT	TRANSEMM 583 602	DR EMBL; M57912; AAA99050.1;			
FT	DOMAIN 603 617	DR Flybase; FBgn012512; Dmav\mt; ND2.			
FT	TRANSEMM 618 636	DR InterPro; IPR003917; NADHub_oxred2.			
FT	DOMAIN 637 644	DR InterPro; IPR003916; NADHub_oxred5.			
FT	TRANSEMM 645 663	DR InterPro; IPR001750; NADHub_oxred5.			
FT	DOMAIN 664 673	DR Pfam; PF00361; oxidore_91; 1.			
FT	TRANSEMM 674 692	DR PRINTS; PR01436; NADHDICASES2.			
FT	DOMAIN 693 711	DR PRINTS; PR01434; NADHDICASES.			
FT	TRANSEMM 712 732	DR Oxidoreductase; NAD; Ubi quinone; Mitochondrion; Transmembrane.			
FT	DOMAIN 733 786	FT NON_TER 1			
FT	TRANSEMM 787 811	FT SEQUENCE 274 AA; 3226 MW; BB27336F88ED40B CRC64;			
FT	DOMAIN 812 945	Query Match 7.3%; Score 88; DB 1; Length 274;			
FT	TRANSEMM 946 964	Best Local Similarity 21.0%; Pred. No. 1.1;			
FT	DOMAIN 965 980	Matches 37; Conservative 29; Mismatches 56; Indels 54; Gaps 6;			
FT	TRANSEMM 981 1000	Query 28 LGVWYLIINAVVLLILLSSALADPDQYNN--FSS-SERGGDFFEMDDANMCTIAISL 80			
Query	7.4%; Score 88.5; DB 1; Length 2203;	DR 77 LNKKLILLISVILSITIGGLNQTSLRKLMASINFLGW--MLSS 122			
Matches	Best Local Similarity 25.0%; Pred. No. 7.8; Mismatches 61; Indels 43; Gaps 10;	DR 81 LMILICAMATGGAYKORAWIIPPFYCQIFDFALMMLVAITVLYPPNSIOQEY-----132			
Db	21 VRTGTLILLGVVLLILNAVVLILLSSAL--DP-DQYNSSESLG-GDFEFMDANMCI 74	Db 123 LMI-----SESTWLYPPFYSFSFVTFMENFKLPHNLQSWYNSKILK 170			
Db	934 IRVGCKLILNHRHTMLLIVTMLSSAALAAEDPFRSHSFRNTLGYFDAF-----985	Db 133 -----IRQLPPNPFPYRDDVNSVNPTCL---VLLILFISILTFKGYLYLIS 175			
Qy	75 AIAISLMLICAMATGGAYKORAWIIPPFYCQIFDFALMMLVAITVLYPPNSIOQEYIR 134	Db 171 FTLFNNFLSLGGFLPKWNLVIQQLTLCNQFLLMMMMSTLITLFFYLRLIC 226			
Db	986 -TAIFVTEILL-KM7TGFALHKGA----FCRNTFNL-LDMLVVGVLV-----1027	RESULT 15			
Qy	135 QLPPNPFPYRDDVNSVNPTCL---VLLILFISILTFKGYLYLIS 192	MTR_NEUCR			
Db	1028 ----SFGIQSASSVVKLRLVRPLRAINRAGLKHVVQCVFVAITI-----GNIM 1078	ID MTR_NEUCR			
Qy	193 VVTT 196	AC P3880;			
Db	1079 IVTT 1082	DT 01-FEB-1995 (Rel. 31, Created)			
Qy	15 SEP-2003 (Rel. 42, Last annotation update)	DT 01-NOV-1997 (Rel. 35, Last sequence update)			
Db	N amino acid transport system protein (Methytryptophan resistance protein).	DE DE Protein).			
GN	MTR.	GN			
RESULT 14					

OS Neurospora crassa; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariaceae; Neurospora.
 OC NCBI_TaxID=5141;
 OX [1]
 RP SEQUENCE FROM N.A.
 STRAIN=Oak Ridge;
 MEDLINE=950505; PubMed=8001794;
 RX Dillon D., Stadler D.;
 RA "Spontaneous mutation at the mtr locus in neurospora: the molecular spectrum in wild-type and a mutator strain.,"
 RT Genetics 138:61-74 (1994).
 RL [2]
 RP SEQUENCE OF 210-470 FROM N.A.
 RX MEDLINE=92146948; PubMed=1838345;
 RA Koo K., Stuart W.D.;
 RT "Sequence and structure of mtr, an amino acid transport gene of
 RT Neurospora crassa,"
 RL Genome 34:644-651 (1991).
 CC -!- FUNCTION: REQUIRED FOR THE TRANSPORT OF NEUTRAL ALIPHATIC AND
 AROMATIC AMINO ACIDS VIA THE N SYSTEM.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to the amino acid/polyamine transporter family
 CC II.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 DR EMBL; L34405; AAA33600.1; -.
 DR EMBL; S81567; AAB21410.1; -.
 DR PIR; S4782; S47892.
 DR InterPro; IPR002422; AA/rel_permease2.
 DR Pfam; PF01490; Aa_trans_1.
 KW Transport; Amino-acid transport; Transmembrane.
 FT DOMAIN 1 56 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 57 77 POTENTIAL.
 FT TRANSMEM 78 98 POTENTIAL.
 FT DOMAIN 99 131 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 132 152 POTENTIAL.
 FT DOMAIN 153 168 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 169 189 POTENTIAL.
 FT TRANSMEM 191 211 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 212 236 POTENTIAL.
 FT TRANSMEM 237 257 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 258 275 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 276 296 POTENTIAL.
 FT DOMAIN 297 316 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 317 337 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 338 357 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 358 378 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 379 386 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 387 407 POTENTIAL.
 FT DOMAIN 408 427 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 428 448 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 449 470 CYTOPLASMIC (POTENTIAL).
 SQ SEQUENCE 470 AA; 51162 MW; E8132D1A62373300 CRC64;
 Query Match 7.3%; Score 87.5%; DB 1; Length 470;
 Best Local Similarity 18.3%; Pred. No. 2;
 Matches 41; Conservative 44; Mismatches 64; Indels 75; Gaps 10;
 Qy 20 HVRGTGILGV-----WLIINAVLILSALADPQDNFSESELGDFEFMDANM 72
 Db 148 HVLGTGIMWGTTIDNGNTCSLVLGVIVSAILFLAIPP-SFARVAIIG--YIDFVSI 202
 Qy 73 CIAATSLIMLICAMATYGAYKORAAMIPEFFCYQIFDFAL-NMLVATVLYPNSTG- 130
 Db 203 CAAIITMI----ATGIRSSHQEGLAAVWSCMPKEDLSLAEGLIAVSNIVFAYSFAM 257

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OM protein - protein search, using sw model

Run on: February 2, 2004, 14:19:40 ; Search time 35 Seconds

Perfect score: 1200

Sequence: 1 MKMVAAPTRFYSNSCCLCCH.....YDDATVNGAAKEPPPPYVSA 226

Scoring table: BLOSUM62

GapOp 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPREMBL 23:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriopl:*

17: sp_archaea:*

17 102.5 8.5 Q17664 caenorhabdi

18 101.5 8.5 Q95Q81 caenorhabdi

19 99.5 8.3 Q92T11

20 99.5 8.3 Q95622 sachcharomyces

21 99 8.2 Q045622 actinobacil

22 98.5 8.2 Q05370

23 97.5 8.1 Q9ENQ1

24 96 8.0 Q8119

25 95.5 8.0 Q17550 caenorhabdi

26 94.5 7.9 Q9jj42 rattus norvegicus

27 94 7.9 Q18277 caenorhabdi

28 94 7.8 Q9VZL8 drosophila

29 93.5 7.8 Q855Q4 streptococcus

30 93.5 7.8 Q45310 caenorhabdi

31 93 7.8 Q19757 caenorhabdi

32 91.5 7.6 Q02789 mus musculus

33 91.5 7.6 Q9m878 arribalzaga

34 91 7.6 Q947D5 caulobacter

35 91 7.6 Q9zz28 trichophyton

36 90 7.5 Q8IC29 plasmidium

37 90 7.5 Q9XN18 euglena gracilis

38 89.5 7.5 Q20508 caenorhabdi

39 89.5 7.5 Q8HET6 formica tru

40 89.5 7.5 Q9MGJ3 drosophila

41 89 7.4 Q9VLi3 drosophila

42 89 7.4 Q9Jkt3 mus musculus

43 89 7.4 Q8K98 pseudomonas

44 89 7.4 Q927Z1 listeria in

45 89 7.4 Q8WWZ4 homo sapien

ALIGNMENTS

RESULT 1

Q9H060	PRELIMINARY;	PRT;	226 AA.
ID Q9H060			
AC Q9H060;			
DT 01-MAR-2001 (TREMBLrel. 16, Created)			
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)			
DB Hypothetical protein NTRM1000066 (Putative integral membrane protein 4 beta) (Putative integral membrane transporter)			
DE (Lyosomal-associated transmembrane protein 4 beta)			
DE membrane transporter)			
GN DKF2586EL124 OR LAPTM4BETA.			
OS Homo sapiens (Human)			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX NCBI_TaxID=9606;			
RN [1] _TAXID=9606;			
RP SEQUENCE FROM N.A.			
RC TISSUE=Uterus			
RX MEDLINE=21154817; PubMed=11230166;			
RA Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,			
RA Ansgere W., Becher M., Bloecker H., Bauersachs S., Blum H.,			
RA Lauber J., Duesterhoeft A., Beyer A., Koehler K., Strack N.,			
RA Mewes H.W., Oettwander B., Obermaier B., Tampe J., Heubner D.,			
RA Wambutt R., Korn B., Klein M., Poustka A.;			
RA "Towards a Catalog of Human Genes and Proteins: Sequencing and			
RA Analysis of 50 Novel Complete Protein Coding Human cDNAs.,"			
RA Genome Res. 11:422-435 (2001).			
RA [2] _			
RA SEQUENCE FROM N.A.			
RA Shao G., Zhou R.;			
RI Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.			
RA [3] _			
RT TISSUE FROM N.A.			
RT SEQUENCE FROM N.A.			
RC TISSUE=Eye;			
RC Strasbourg R.;			
RA Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.			
RI [4] _			
RP SEQUENCE FROM N.A.			
RA Hogue D.L.;			

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	1200	100.0	226	4	Q9H060		O9h060 homo sapien
2	1200	100.0	283	4	Q9NY06		Q9ny06 homo sapien
3	1113.5	92.8	227	11	Q91XQ6		Q9xq66 mus musculus
4	552.5	46.0	233	11	Q8BG66		Q8bg66 mus musculus
5	550.5	45.9	233	4	Q9BTU8		Q9btu8 homo sapien
6	432.5	36.0	197	11	Q9CRX2		Q9crx2 bombyx mori
7	317	26.2	313	5	Q964G6		Q964G6 bombyx mori
8	287.5	24.0	421	5	Q8MMKR3		Q8mmkr3 drosophila
9	287.5	24.0	428	5	Q95R82		Q95r82 drosophila
10	282.5	23.5	432	5	Q9V4X3		Q9v4x3 drosophila
11	170	14.2	261	11	Q9JJ55		Q9jj55 rattus norvegicus
12	157	13.1	286	5	Q9BLM6		Q9blm6 schistosoma
13	156	13.0	261	11	Q8BFZ0		Q8bfz0 mus musculus
14	146.5	12.2	281	5	Q9U597		Q9u597 schistosoma
15	122	10.2	165	5	Q9VEW3		Q9vev3 drosophila
16	115	9.6	236	5	Q23190		Q23190 caenorhabdi

RC	SEQUENCE FROM N.A.
RA	Hogue D.L.;
RA	"Functional annotation of a full-length mouse cDNA collection.";
RT	Submitted (Oct-2000) to the EMBL/GenBank/DBJ databases.
RL	EMBL; AF317420; AAK69528.1; -.
DR	InterPro: IPI004607; MspI.
DR	Pfam: PF03821; MspI. 1.
DR	Transmembrane.
SQ	SEQUENCE 313 AA; 34292 MW; 52CB6D97E0DB71C3 CRC64; [6]
RP	Query Match 26.2%; Score 315; DB 5; Length 313;
RP	Best Local Similarity 29.0%; Pred. No. 1.4e-22;
RP	Matches 76; Conservative 47; Mismatches 79; Indels 60; Gaps 8;
Qy	15 CCLCCHVVRTGTTIIGWVLLINAVVLLILSALADP---DOYNFSSELG-----GD 63
Db	18 CCFCUHVVRTGTTIIGSWHFLVAGVAAIVDPRLLDESSPVSSWNVGRGD 77
Qy	64 F-----EFMDAMCIAIAISLMLICAMATGAYKORAAWIPE 104
Db	78 VLPPRLSNTVERTRSPSYOASHPSDLSYLGLMALTMI---YGARGRPAYLLPF 132
Qy	105 PCYQFDALINMLVATVLYPNISIQEYIROLPPNPYPRDDVMSVNPTCLVLVLLFISI 164
Db	133 FCLQIDFADITLTATGCLCYLROHALIAE---TRVPPREELLRPAPALLAFVVISALIV 191
Qy	165 ILTFKGYLISCVNWCNTRYINGRNSS---DVLVYTSNDTTV-----LL 204
Db	192 AVITKGYCVSVWRCKLTMRITALQSLTPVTSIDGIVTSAPPYFQOPATPDYSSL 251
Qy	205 PPDYDATVGAKEPPPPVSA 226
Db	252 PDYEA---VKQTPPPSYRAA 269
RESULT 8	
Q8MFR3	Q8MFR3 PRELIMINARY; PRT; 421 AA.
ID	Q8MFR3; PRT; 421 AA.
AC	Q8MFR3; PRELIMINARY; PRT; 421 AA.
DT	01-OCT-2002 (TREMBrel. 22, Created)
DT	01-OCT-2002 (TREMBrel. 22, Last sequence update)
DT	01-MAR-2003 (TREMBrel. 23, Last annotation update)
DE	CG14767-PA.
GN	CG14767 OR CG8575.
OS	Drosophila melanogaster (Fruit fly).
OC	Eutaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriodea; Drosophilidae; Drosophila.
OC	[1]
RN	[1]_TaxID:PD227;
RP	SEQUENCE FROM N.A.
RC	ST281N=Berkeley;
RA	Medline=20196006; PubMed=10731132;
RA	Adams M.D., Celiker S.B., Holt R.A., Evans C.A., Gocayne J.D.,
RA	Amaratides P.G., Scheer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA	Sutton G.G., Wortman J.R., Yandell M., Zhang Q., Chen L.X.,
RA	Brandon R.C., Rogers Y.-H.C., Blazej R.G., Chame P., Pfeiffer B.D.,
RA	Wan K.H., Doyle C., Baxter B.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA	Abrial J.-F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley B.M.,
RA	Beezon K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA	Burris K.C., Busam D.A., Butler H., Cadieu E., Chandra I.,
RA	Cherry J.M., Cowley S., Dahlke C., Davenport L.B., Davies P.,
RA	de Fablos B., Deicher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunn P.,
RA	Durbin R.J., Evangelista C.C., Ferreria S., Fleischmann W.,
RA	Poser C., Gabrilian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA	Gloek A., Geng F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA	Hobson D., Houston K.A., Howland T.J., Wei M.-H., Ikegami C.,
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

GN CG14767 OR CG8575.	QY 70 -----	----- ANMCIAIAISLMLICAMATYGAYKORAATWI 102
OS Drosophila melanogaster (Fruit fly).	Db 95 PALPTPLSKVEPPYARDHSALNRYKRKYONEDIGGLVCTCMIAITLMLIYGTIGKPSHDL 154	
ECU Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
CC Drosophilidae; Drosophila; Drosophila.		
NCBI TaxID:7227;		
[1]		
RN SEQUENCE FROM N.A.		
STRAIN=BERKELEY;		
RC MEDLINE=20196006; PubMed=10731132;		
RA Adams M.D., Celikin S.B., Evans C.A., Gocayne J.D.,	QY 95 PALPTPLSKVEPPYARDHSALNRYKRKYONEDIGGLVCTCMIAITLMLIYGTIGKPSHDL 162	
RA Amanatidis P.G., Scherer S.E., Li P.W., Hopkins R.A., Galle R.F.,	103 PPFCCYQIDPFLANMLVAITVLVYPNISDIBYIROLPPNPYRDDVMSVNPPTCLVLILIF1 162	
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,	155 PPFCLQLQDRAFTLTLTAAGYLCVQLQATHSIIAE-SHRLPWERKLELPPEELVWVLVVF 213	
RA Sutton G.G., Wormtall M.D., Zhang Q., Chen L.X.,	163 SIIITFKSYLISCVWNCYRYI ----- NGRNSSDVLYVYTSNDTIVLPP 205	
RA Brandon R.C., Rogers Y.H.C., Blaizej R.G., Champe M., Pfeiffer B.D.,		
RA Wan K.H., Doyle C., Baxter F.G., Helt G., Nelson C.R., Miklos G.L.G.,		
RA Abril J.F., Agbayani A., An H.-J., Andrews P.-Fankoch C., Baldwin D.,		
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley B.M.,		
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,	QY 214 ICIVFLKAYCIGIVWRCKYLTRQHQVRLFPFLEPPGTVHSVGGTGAERSYSTLLP 273	
RA Burkova D., Botchan M.R., Bouck J., Broctier P.,	Db 206 PYDADTVNGAAKEKPPPPY 223	
RA Burriss K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,	274 NYDEIAQYLQKAPPSSY 291	
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,		
RA de Pablos D., Delcher A., Dang Z., Mayr A.D., Dew I., Diez S.M.,	QY 215 Created	
RA Dodson K., Doub L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,	DT 01-OCT-2000 (TREMBLrel.	
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,	DT 01-OCT-2002 (TREMBLrel.	
RA Fobler A., Gabrielson A.E., Garg N.S., Geller W.M., Glasser K.,	DT 01-OCT-2002 (TREMBLrel.	
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,	DE GCD-10.	
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houch J.,	GN Rattus norvegicus (Rat).	
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,	OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,	OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,	NCBI_TaxID=10116;	
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,	RN	
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,	RP SEQUENCE FROM N.A.	
RA Merkulov G., Mil'shina N.V., Mobarry C., Morris J., Moshrefi A.,	RX MEDLINE=21192472; PubMed=11295227;	
RA Mount S.M., Moy M., Murphy L., Muzny D.M., Nelson D.L.,	RA Origasa M., Tanaka S., Suzuki K., Tone S., Lim B., Koike T.,	
RA Nelson D.R., Nelson K.A., Nixon L., Nusskern D.R., Pacleb J.M.,	RT RT Activation of a Novel Microglial Gene Encoding a Lysosomal Membrane	
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,	RT Protein in Response to Neuronal Apoptosis.;"	
RA Reinert K., Remington K., Saunders R.D.C., Scheeler P., Shen H.,	RL Mol. Brain Res. 88:1-13 (2001).	
RA Shue B.C., Sieden-Klamos I., Saunders R., Simpson M., Skupski M.P., Smith T.,	DR EMBL; AB046592; BAB034511; -.	
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,	DR InterPro; IPR046577; Mtp.	
RA Svärsks R., Tector C., Turner R., Venter J.C., Wang A.H., Wang X.,	DR Pfam; PF03821; Mtp; 1.	
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,	DR TIGRFAMS; TIGR00739; mtp; 1.	
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,	SQ 261 AA; 29631 MW; 4C2FEABCBE214DDE CRC64;	
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,	DR TIGRFAMS; TIGR00739; mtp; 1.	
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.C.,	DR TIGRFAMS; TIGR00739; mtp; 1.	
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,	DR TIGRFAMS; TIGR00739; mtp; 1.	
RT "The genome sequence of <i>Drosophila melanogaster</i> .";	DR TIGRFAMS; TIGR00739; mtp; 1.	
RL <i>Science</i> 287:2185-2195 (2000).	DR TIGRFAMS; TIGR00739; mtp; 1.	
RN [2]	DR TIGRFAMS; TIGR00739; mtp; 1.	
RP SEQUENCE FROM N.A.	DR TIGRFAMS; TIGR00739; mtp; 1.	
RA Hogue D.L.;	DR TIGRFAMS; TIGR00739; mtp; 1.	
RT "Identification of a LAPTM ortholog in <i>Drosophila melanogaster</i> .";	DR TIGRFAMS; TIGR00739; mtp; 1.	
RL Submitted (OCT 2000) to the EMBL/GenBank/DBJ databases.	DR TIGRFAMS; TIGR00739; mtp; 1.	
CC -1 ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A	DR TIGRFAMS; TIGR00739; mtp; 1.	
CC SHORT FORM: ARE PRODUCED BY ALTERNATIVE SPLICING.	DR TIGRFAMS; TIGR00739; mtp; 1.	
DR EMBL; AE003836; AF059049; -.	DR TIGRFAMS; TIGR00739; mtp; 1.	
DR AF059049; -.	DR TIGRFAMS; TIGR00739; mtp; 1.	
DR AF171419; AF069597; -.	DR TIGRFAMS; TIGR00739; mtp; 1.	
DR FlyBase; FBgn0040777; CG14767.	DR TIGRFAMS; TIGR00739; mtp; 1.	
DR InterPro; IPR004687; Mtp.	DR TIGRFAMS; TIGR00739; mtp; 1.	
DR Pfam; PF03821; Mtp; 1.	DR TIGRFAMS; TIGR00739; mtp; 1.	
KW Alternative splicing; Transmembrane;	DR TIGRFAMS; TIGR00739; mtp; 1.	
VARSPLIC 1 MISSING (IN SHORT ISOFORM).	DR TIGRFAMS; TIGR00739; mtp; 1.	
SEQUENCE 432 AA; 47609 MW; ADB00C036EC74C4 CRC64;	QY 207 YDDA----TVNGAAKEPPPPY 223	
Query Match 23.5%; Score 282.5; DB 5; Length 432;	Db 238 YEEAISLPTKTPPEGDAPPY 258	
Best Local Similarity 26.4%; Pred. No. 3.1e-19;		
Matches 68; Conservative 40; Mismatches 97; Indels 53; Gaps 5;		
RESULT 12		
Q9BIM6		
Q9BIM6		
AC Q9BIM6;	PRELIMINARY;	PRT; 286 AA.
DT 01-JUN-2001 (TREMBLrel. 17, Created)		

DT	01-JUN-2001	(TrEMBLrel. 17, Last sequence update)	Qy	74 IAIASLL---MILICAMATYGAYKORAIIPIFFCYQIFDEALNMVIAITVLIYPNSTQ	130
DT	01-DEC-2002	(TrEMBLrel. 22, Last annotation update)	Db	62 DLISSFLILIGVLFISIISLPGVNRXYLIPPLSLQIMDFLCLLTLGTSI---EUP	118
DE	Trispanning orphan receptor.				
GN	TM3				
OS	Schistosoma haematochium (Blood fluke)				
OC	Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidaida;				
SC	Schistosomatidae; Schistosomatidae; Schistosoma.				
NCBI_TaxID	6185;				
[1]					
RN	SEQUENCE FROM N.A.				
RA	MEDLINE=9926361; PubMed=10366712;				
InaL J.M.;					
RT	"Schistosoma TOR (trispanning orphan receptor), a novel, antigenic				
surface receptor of the blood dwelling, Schistosoma parasite."					
RL	Biochim. Biophys. Acta 1445:183-208(1999).				
DR	EMBL; U57714; AAK11492.1; -.				
KW	Receptor.				
SQ	SEQUENCE 286 AA; 31755 MW; A188B2046289c248 CRC64;				
	Query Match 13.1%; Score 157; DB 5; Length 286;				
	Best Local Similarity 21.6%; Pred. No. 3.1e-07;				
Matches 43; Conservative 29; Mismatches 69; Indels 58; Gaps 4;					
	AC Q9U597; PRELIMINARY; PRT; 281 AA.				
Qy	74 IAIASLLMILICAMATYGAYKORAIIPIFFCYQIFDEALNMVIAITVLIYPNSTQ	133			
Db	28 IAVCVTTPLAFCFMVHAAITRQPTHLPPFQVDFLICLILHGFMSTSDIRLWV	87			
Qy	134 RQLPPNFPYRDDVMSVNPCTVLVILIFISTILTPKGYLJSCWNCYRIT-----	183			
Db	88 HT-----KIGPIYTKSTGTLTFLISICMMLAFKAYCLGMVWIDCYKTYLMLNRGNLJLD	140			
Qy	184 -----NGRNS-----	205			
Db	141 DWYSDQWGHLSLTSWLSLRTGRNRGNNSIGNSGSPNBPNTPRPDTITYDFAND---LPK	196			
Qy	207 YDDATVNGAAKEPPPPYVS	225			
Db	197 YEDIKIRINAYAPPYCS	215			
	RESULT 14				
Q9U597	PRELIMINARY; PRT; 281 AA.				
Q9U597	AC Q9U597; PRELIMINARY; PRT; 281 AA.				
Q9U597	DT 01-MAY-2000 (TREMBLrel. 13, Created)				
Q9U597	DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)				
Q9U597	DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)				
	DE Trispanning orphan receptor.				
	OS Schistosoma mansoni (Fluke).				
	OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidaida;				
	OC Schistosomatidae; Schistosomatidae; Schistosoma.				
	RN [1]; NCBI_TaxID=6183;				
	SEQUENCE FROM N.A.				
	RA Inai, J.M.;				
	RT "Schistosoma TOR (trispanning orphan receptor), a novel, antigenic				
	surface receptor of the blood-dwelling, Schistosoma parasite."				
	RL Biochim. Biophys. Acta 1445:183-208(1999).				
	DR EMBL; AF051138; AAF21676.1; -.				
	KW Receptor.				
	SQ SEQDBNCE 281 AA; 31060 MW; BADA7B91E9DB9BS CRC64;				
	Query Match 12.2%; Score 146.5; DB 5; Length 281;				
	Best Local Similarity 20.5%; Pred. No. 3.2e-06;				
Matches 41; Conservative 33; Mismatches 67; Indels 59; Gaps 5;					
	AC Q9U597; PRELIMINARY; PRT; 281 AA.				
Qy	74 IAIASLLMILICAMATYGAYKORAIIPIFFCYQIFDEALNMVIAITVLIYPNSTQ	133			
Db	28 IAVCVTTPLAFCFMVHAAITRQPTHLPPFQVDFLICLILHGFMSTSDIRLWV	87			
Qy	134 RQLPPNFPYRDDVMSVNPCTVLVILIFISTILTPKGYLJSCWNCYRIT-----	183			
Db	88 HT-----KIGPIYTKSTGTLTFLISICMMLAFKAYCLGMVWIDCYKTYLMLNRGNLJLD	140			
Qy	184 -----NGRNS-----	205			
Db	141 DWYSDQWGHLSLTSWLSLRTGRNRGNNSIGNSGSPNBPNTPRPDTITYDFAND---LPK	196			
Qy	207 YDDATVNGAAKEPPPPYVS	225			
Db	197 YEDIKIRINAYAPPYCS	215			
	RESULT 15				
Q9VW3	PRELIMINARY; PRT; 165 AA.				
Q9VW3	AC Q9VW3; PRELIMINARY; PRT; 165 AA.				
Q9VW3	DT 01-MAY-2000 (TREMBLrel. 13, Created)				
Q9VW3	DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)				
Q9VW3	DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)				
	DB CG10311 protein (R8619p).				
	GN CG10311.				
	OS Drosophila melanogaster (Fruit fly).				
	OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Muscomorpha;				
	OC Neoptera; Endopterygota; Diptera; Neoptera;				
	Db 14 SCCLCCHVRTGILGWLILINAVVLLILSALADPQDNFNSSESLGGGEEFMDANMC 73				
	Db 15 TCC-CFNRVATIAYHMWS-VLFLFTHVV----EVARGKVCRRFKMPYLRMA 61				

OC Ephydriidea; Drosophilidae; Drosophila.
 OC [1] _TAXID=7227;
 RN SEQUENCE FROM N.A.

RP STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Calnikter S.E., Holt R.A., Evans C.A., Gocayne J.D., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Horskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Galle R.F.,
 RA Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champé M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter F.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borikova D., Botchan M.R., Bouck J., Brokstein P., Brortier P.,
 RA Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin R.K.J., Evangelista C.C., Ferraz C., Ferrira S., Fleischmann W.,
 RA Fosler C., Gabrielson A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke J., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Nobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclob J.M.,
 RA Palazzo M., Pitman G.S., Pan S., Pollard J., Puris V., Reese M.G.,
 RA Reiner K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Sieden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spreading A.C., Stimpson M., Strong R., Sun E., Wang X.,
 RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong W.H., Zhou X., Zou X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195 (2000).
 RN [2]
 RP SEQUENCE FROM N.A.

SEQUENCE FROM N.A.
 RP STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Calnikter S.E., Holt R.A., Evans C.A., Gocayne J.D., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Horskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Galle R.F.,
 RA Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champé M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter F.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borikova D., Botchan M.R., Bouck J., Brokstein P., Brortier P.,
 RA Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin R.K.J., Evangelista C.C., Ferraz C., Ferrira S., Fleischmann W.,
 RA Fosler C., Gabrielson A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke J., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Nobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclob J.M.,
 RA Palazzo M., Pitman G.S., Pan S., Pollard J., Puris V., Reese M.G.,
 RA Reiner K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Sieden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spreading A.C., Stimpson M., Strong R., Sun E., Wang X.,
 RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong W.H., Zhou X., Zou X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195 (2000).
 RN [2]
 RP SEQUENCE FROM N.A.

SEQUENCE FROM N.A.
 RP STRAIN=BERKELEY;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Carlson J.,
 RA Chame M., Chavez C., Dorsett V., Dreaneck D., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guarin H., Kromiller B., Li P., Liao G.,
 RA Miranda A., Mongall C.J., Munoo J., Paragis V., Park S.,
 RA Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celikker S.;
 RA Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE003713; AE05304.1; -.
 DR EMBL; AE11535; AE029540.1; -.
 DR EMBL; AE0038430; CG10311;
 DR EMBL; AE0038430; CG10311; 18683 MW; E139A945120A343 CRC64;
 SQ SEQUENCE 165 AA; 18683 MW; E139A945120A343 CRC64;
 QY 10 - - - - - Query Match 10.2%; Score 122; DB 5;
 DB Best Local Similarity 21.7%; Pred. No. 0.00045;
 DB Matches 40; Conservative 42; Mismatches 56; Indels 46; Gaps 7;
 DB 7 NSCCUCCHVWTGTLLIGWWLILNLSSALADPDQYNSSESELGCDFTMDD-- 69
 DB 7 NSCCUCQSTANGSVSGLIAVLISSTTIVFTT----RVHFKTII---IFDFIPNDIV 57
 QY 70 - - - - - 124 ANMCTAIAISLIMILICAMATYGAQKQRAWIIPFCYQIFDFALNLMLVATVLI
 QY 58 KIIILVTLNLCMTILSHMLII-----GALKKRNHTYLMVPN-----VVGIMTAIGLII 103
 DB 125 YPN51QBYT1RQLPPNPFYRDDVMSVNPCTCLVLI-LLFPSIILTPKGYLLISCVNCYRVI 183
 QY 58 KIIILVTLNLCMTILSHMLII-----GALKKRNHTYLMVPN-----VVGIMTAIGLII 103

Result No.	Score	Query	Match	Length	DB	ID	Description
1	1200	100.0	226	21	AAY94879		Human protein clon
2	1200	100.0	226	22	ABU5220		Human intracellular
3	1200	100.0	226	22	AAM39575		Human polypeptide
4	1200	100.0	226	22	AAB74720		Human membrane ass
5	1200	100.0	226	22	AAB88317		Human membrane or
6	1200	100.0	226	23	ABBB9618		Human polypeptide
7	1200	100.0	226	24	AABU6391		Lung cancer-assoc
8	1200	100.0	231	24	AAM41761		Human polypeptide
9	1200	100.0	283	23	ABP64704		Human protein SEQ

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	1200	100.0	226	21	AAY94879		Human protein clon
2	1200	100.0	226	22	ABU5220		Human intracellular
3	1200	100.0	226	22	AAM39575		Human polypeptide
4	1200	100.0	226	22	AAB74720		Human membrane ass
5	1200	100.0	226	22	AAB88317		Human membrane or
6	1200	100.0	226	23	ABBB9618		Human polypeptide
7	1200	100.0	226	24	AABU6391		Lung cancer-assoc
8	1200	100.0	231	24	AAM41761		Human polypeptide
9	1200	100.0	283	23	ABP64704		Human protein SEQ

ALIGNMENTS

RESULT 1	AAY94879	
ID	AAY94879	standard; Protein; 226 AA.
XX		
		Human protein; hydrophobic domain; nutritional source; haematopoiesis; cytokine production; cell proliferation; cell differentiation; immune deficiency; infectious disease; autoimmune disorder; asthma; multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis; osteoporosis; osteoarthritis; periodontal disease; allergic reaction; nervous system disorder; Alzheimer's disease; Parkinson's disease; Huntington's disease; liver fibrosis; lung fibrosis; reperfusion injury; coagulation disorder; myocardial infarction; inflammatory condition; septic shock; sepsis; ischaemia; reperfusion injury; arthritis; tumour; nephritis; therapy.
		Homo sapiens.

Human protein clone

Human intracellular

Human polypeptide

Human membrane assay

Human membrane or

Human polypeptide

Lung cancer-associated

Human polypeptide

Human protein SEQ

Human protein clon

Human intracellular

Human polypeptide

Human membrane assay

Human membrane or

Human polypeptide

Lung cancer-assoc

Human polypeptide

Human protein SEQ

Human protein clon

Human intracellular

Human polypeptide

Human membrane assay

Human membrane or

Human polypeptide

Human protein SEQ

Human protein clone

Human intracellular

Human polypeptide

Human membrane assay

Human membrane or

Human polypeptide

Lung cancer-associated

Human polypeptide

Human protein SEQ

Human protein clon

Human intracellular

Human polypeptide

Human membrane assay

Human membrane or

Human polypeptide

Lung cancer-assoc

Human polypeptide

Human protein SEQ

Human protein clon

Human intracellular

Human polypeptide

Human membrane assay

Human membrane or

Human polypeptide

Human protein SEQ

Human protein clone

Human intracellular

Human polypeptide

Human membrane assay

Human membrane or

Human polypeptide

Lung cancer-associated

Human polypeptide

Human protein SEQ

Human protein clon

Human intracellular

Human polypeptide

Human membrane assay

Human membrane or

Human polypeptide

Lung cancer-assoc

Human polypeptide

Human protein SEQ

Human protein clon

Human intracellular

Human polypeptide

Human membrane assay

Human membrane or

Human polypeptide

Human protein SEQ

Human protein clone

Human intracellular

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Human membrane assay

Human membrane or

Human polypeptide

Lung cancer-associated

Human polypeptide

Human protein SEQ

Human protein clon

Human intracellular

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Human membrane assay

Human membrane or

Human polypeptide

Lung cancer-assoc

Human polypeptide

Human protein SEQ

Human protein clon

Human intracellular

Human polypeptide

Human membrane assay

Human membrane or

Human polypeptide

Human protein SEQ

Human protein clone

Human intracellular

Human polypeptide

Human membrane assay

Human membrane or

Human polypeptide

Lung cancer-associated

Human polypeptide

Human protein SEQ

Human protein clon

Human intracellular

Human polypeptide

Human membrane assay

Human membrane or

Human polypeptide

Lung cancer-assoc

Human polypeptide

Human protein SEQ

Human protein clon

Human intracellular

Human polypeptide

Human membrane assay

Human membrane or

Human polypeptide

Human protein SEQ

Human protein clone

Human intracellular

Human polypeptide

Human membrane assay

Human membrane or

Human polypeptide

Lung cancer-associated

Human polypeptide

Human protein SEQ

Human protein clon

Human intracellular

Human polypeptide

Human membrane assay

Human membrane or

Human polypeptide

Lung cancer-assoc

Human polypeptide

Human protein SEQ

Human protein clon

Human intracellular

Human polypeptide

Human membrane assay

Human membrane or

Human polypeptide

Human protein SEQ

Human protein clone

Human intracellular

Human polypeptide

Human membrane assay

Human membrane or

Human polypeptide

Lung cancer-associated

Human polypeptide

Human protein SEQ

Human protein clon

Human intracellular

Human polypeptide

Human membrane assay

Human membrane or

Human polypeptide

Lung cancer-assoc

Human polypeptide

Human protein SEQ

Human protein clon

Human intracellular

Human polypeptide

Human membrane assay

Human membrane or

Human polypeptide

Human protein SEQ

Human protein clone

Human intracellular

Human polypeptide

Human membrane assay

Human membrane or

Human polypeptide

Lung cancer-associated

Human polypeptide

Human protein SEQ

Human protein clon

Human intracellular

Human polypeptide

Human membrane assay

Human membrane or

Human polypeptide

Lung cancer-assoc

Human polypeptide

Human protein SEQ

Human protein clon

Human intracellular

Human polypeptide

Human membrane assay

Human membrane or

Human polypeptide

Human protein SEQ

Human protein clone

Human intracellular

Human polypeptide

Human membrane assay

Human membrane or

Human polypeptide

Lung cancer-associated

Human polypeptide

Human protein SEQ

Human protein clon

Human intracellular

Human polypeptide

Human membrane assay

Human membrane or

Human polypeptide

Lung cancer-assoc

Human polypeptide

Human protein SEQ

Human protein clon

Human intracellular

Human polypeptide

Human membrane assay

Human membrane or

Human polypeptide

Human protein SEQ

Human protein clone

Human intracellular

Human polypeptide

Human membrane assay

Human membrane or

Human polypeptide

Lung cancer-associated

Human polypeptide

PR 25-AUG-1998; 98JP-0238116.
 PR 09-SEP-1998; 98JP-0254736.
 PR 29-SEP-1998; 98JP-0275505.
 XX (SAGA) SAGAMI CHEM RES CENT.
 PA (PROT) PROGENE INC.
 XX
 PI Kato S, Kimura T;
 XX
 DR; WPI; 2000-182694/16.
 XX
 Novel human proteins having hydrophobic domains useful for treating osteoporosis, Alzheimer's disease, Parkinson's disease, asthma, multiple sclerosis, rheumatoid arthritis, cancer, anaemia, and stroke -
 XX
 PS Claim 1; Page 275-276; 351pp; English.
 XX
 This sequence represents a human protein of the invention, which has hydrophobic domains. The DNA sequences can be used as a probe or as a genetic marker. The protein can also be used as a marker, and to identify potential genetic disorders. The DNA and protein can also be used as nutritional sources or supplements. The protein exhibits cytokine, cell proliferation, cell differentiation activities and induces production of other cytokines in certain cell populations. The protein also exhibits immune stimulating or immune suppressing activity. It can be used in the treatment of various immune deficiencies and disorders, and to treat infectious diseases caused by viral, bacterial, fungal or other infections. The protein is also used for treating autoimmune disorders such as multiple sclerosis, systemic lupus erythematosus, and rheumatoid arthritis. It is also useful in the treatment of allergic reactions and conditions such as asthma, and in immune suppression after organ transplantation. The protein is useful in regulation of hematopoiesis and consequently in the treatment of myeloid or lymphoid cell deficiencies. It is also used in compositions for tissue growth or regeneration. The protein is also used in the treatment of osteoporosis or osteoarthritis and in the treatment of periodontal disease and other tooth repair processes. The protein is used in the treatment of nervous system disorders such as Alzheimer's disease, Parkinson's disease, and Huntington's disease. They are useful for protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage. They are also used for promoting or inhibiting tissue differentiation. They are also used as contraceptives since they exhibit activin or inhibin related activities and as a fertility inducing therapeutic. They are used for treating various coagulation disorders and in treatment and prevention of conditions resulting from coagulation activities e.g. myocardial infarction or stroke. They also act as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. They are used to treat inflammatory conditions such as septic shock, sepsis, ischaemia/reperfusion injury, arthritis, and nephritis. They can be used to prevent tumours.
 XX
 Sequence 226 AA;
 Query Match 100.0%; Score 1200; DB 21; Length 226;
 Best Local Similarity 100.0%; Pred. No. 2.4e-125;
 Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MKMVAAPWTRFYSNSCCCLCHVRTGTLGWYLINAVVLLISALADPDQYNFSSSEL 60
 Db 1 MKMVAAPWTRFYSNSCCCLCHVRTGTLGWYLINAVVLLISALADPDQYNFSSSEL 60
 Qy 61 GGDFFEMDDAMNCIAIAISLMLICAMATYGAJKORAVIIPFFCYQIFDFALNMLVAI 120
 Db 61 GGDFFEMDDAMNCIAIAISLMLICAMATYGAJKORAVIIPFFCYQIFDFALNMLVAI 120
 Qy 121 TVLIPNSIQEYIROLPPNPYRDDMSNPTCLVLLFISIILTFCYGLISCVWNCY 180
 Db 121 TVLIPNSIQEYIROLPPNPYRDDMSNPTCLVLLFISIILTFCYGLISCVWNCY 180
 Qy 181 RYINGRNSSDVLYVYTSDNPTTVLPPYDADTVNGAAKEPPPPYSA 226
 Db 181 RYINGRNSSDVLYVYTSDNPTTVLPPYDADTVNGAAKEPPPPYSA 226
 RESULT 3
 AAM39575

RESULT 2
 ABU52920 standard; Prototin; 226 AA.
 ID ABU52920
 XX
 AC ABU52920;
 XX
 DT 14-APR-2003 (first entry)
 XX
 Human intracellular transport and trafficking protein DKFzphute1_24e11.
 DE XX
 KW Human; gene therapy; vaccine; disease treatment; detection.
 XX
 OS Homo sapiens.
 XX
 PN WO200112659-A2.
 XX
 PD 22-FEB-2001.
 PF 18-AUG-2000; 20000W0-IB01496.
 XX
 PR 18-AUG-1999; 99US-019499.
 PR 28-SEP-1999; 99US-0156503.
 XX
 PA (GERU-) GERMAN HUMAN GENOME PROJECT.
 XX
 PT Nucleic acids having the sequences of clones isolated from libraries of different human tissues, useful in recombinant DNA methodologies -
 XX
 PS Claim 21; Page 534; 1095pp; English.
 XX
 CC This invention describes novel polynucleotides and polypeptides isolated from human cDNA libraries which can be used for gene therapy or in vaccines. The polynucleotides of the invention and antibodies encoded by CC associated with inappropriate polypeptide expression. The products of the invention may also be used to identify modulators of expression and activity and to down regulate expression and activity. The antibodies of the invention may also be used as diagnostic agents for detecting the presence of polypeptides in samples. This sequence represents a CC polypeptide described in the disclosure of the invention.
 XX
 SQ Sequence 226 AA;
 Query Match 100.0%; Score 1200; DB 22; Length 226;
 Best Local Similarity 100.0%; Pred. No. 2.4e-125;
 Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKMVAAPWTRFYSNSCCCLCHVRTGTLGWYLINAVVLLISALADPDQYNFSSSEL 60
 Db 1 MKMVAAPWTRFYSNSCCCLCHVRTGTLGWYLINAVVLLISALADPDQYNFSSSEL 60
 Qy 61 GGDFFEMDDAMNCIAIAISLMLICAMATYGAJKORAVIIPFFCYQIFDFALNMLVAI 120
 Db 61 GGDFFEMDDAMNCIAIAISLMLICAMATYGAJKORAVIIPFFCYQIFDFALNMLVAI 120
 Qy 121 TVLIPNSIQEYIROLPPNPYRDDMSNPTCLVLLFISIILTFCYGLISCVWNCY 180
 Db 121 TVLIPNSIQEYIROLPPNPYRDDMSNPTCLVLLFISIILTFCYGLISCVWNCY 180
 Qy 181 RYINGRNSSDVLYVYTSDNPTTVLPPYDADTVNGAAKEPPPPYSA 226
 Db 181 RYINGRNSSDVLYVYTSDNPTTVLPPYDADTVNGAAKEPPPPYSA 226

ID	AAM39575	Standard; Protein; 226 AA.	QY	61	GGDPFMDANMCTIAAISLIMILICAMATYGAJKQRRAWIIPEFCYQIFDFALNNLVAI	120
AC	AAM39575;		Db	61	GGDPFMDANMCTIAAISLIMILICAMATYGAJKQRRAWIIPEFCYQIFDFALNNLVAI	120
XX	22-OCT-2001	(first entry)	QY	121	TVLIPNSQEVYRQLPPNPYRDDVMSVNPCTLVLLFISLITPGYLISCVNNCY	180
XX	Human polypeptide SEQ ID NO 2720.		Db	121	TVLIPNSQEVYRQLPPNPYRDDVMSVNPCTLVLLFISLITPGYLISCVNNCY	180
KW	Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; hemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; leukaemia.		QY	181	RYINGRNSSDVLYVTSNDTTVLLPYDDATVNGAERPPPTVSA	226
XX	OS Homo sapiens.		Db	181	RYINGRNSSDVLYVTSNDTTVLLPYDDATVNGAERPPPTVSA	226
XX	PN WO200153312-A1.					
XX	PD 26-JUL-2001.					
XX	PF 26-DEC-2000; 2000WO-US34263.					
XX	PR 21-JAN-2000; 2000US-0488725.					
PR 25-APR-2000; 2000US-0552317.						
PR 09-JUL-2000; 2000US-0598442.						
PR 19-JUL-2000; 2000US-0620312.						
PR 03-AUG-2000; 2000US-0653450.						
PR 14-SEP-2000; 2000US-0662191.						
PR 19-OCT-2000; 2000US-0693036.						
PR 29-NOV-2000; 2000US-0727344.						
PA (HYSE-) HYSEQ INC.						
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D; Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;						
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;						
XX WPI: 2001-442253/471.						
DR N-PSDB; AAI58731.						
PT Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -						
PT Example 4: SEQ ID NO 2720; 10078pp; English.						
PS The invention relates to human nucleic acids (AAI57798 AAI61369) and the encoded polypeptides (AAI38642 AAI42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: immune system suppression, actin/inhibit activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.						
CC Note: The sequence data for this patent did not form part of the printed specification.						
XX Sequence 226 AA.						
CC Query Match 100.0%; Score 1200; DB 22; Length 226;						
CC Best Local Similarity 100.0%; Pred. No. 2.4e-125;						
CC Matches 226; Conservative 0; Mismatches 0; Gaps 0;						
QY 1 MKQVAPTRFYSNSCCUCLCHYVRTGTTLGVYLIINAVVLLSALDPQQYNFSSSEL 60						
Db 1 MKQVAPTRFYSNSCCUCLCHYVRTGTTLGVYLIINAVVLLSALDPQQYNFSSSEL 60						

Human membrane associated protein MEMAP-26.

Human; membrane associated protein; MEMAP; diagnosis; cytostatic; antiinflammatory; anticonvulsant; immunosuppressive; antidiarrheic; antiarteriosclerotic; gene therapy; cell proliferative disorder; autoimmune disorder; inflammatory disorder; neurological disorder; neurological and gastrointestinal disorder; cancer; inflammation; atherosclerosis; epilepsy; diarrhoea.

Human membrane associated protein MEMAP.

CC detection of MEMAP protein and can be used as antagonists to treat or
 CC prevent a disorder associated with MEMAP. Polynucleotides encoding MEMAP
 CC can be delivered to target cells with genetic abnormalities with respect
 CC to the expression of MEMAP to treat or prevent a disorder associated
 CC with MEMAP.

can be used in gene therapy. The polymucleotide sequences and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate secretory protein/membrane protein expression. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples. They may also be used to study the expression and function of secretory proteins/membrane polypeptides and their role in metabolism. The polypeptides may be used as antigens in the production of antibodies against them and in assays to identify modulators (agonists and antagonists) of expression and activity. The antibodies and antagonists may also be used as therapeutic agents to down regulate expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of the polypeptides in samples (e.g. by enzyme linked immunosorbant assay (ELISA). Examples of diseases which may be treated include rheumatoid arthritis and diabetes.

		XX	Sequence	226 AA;
b	b	61	GGDFEMDDANCIATAILMLICATYGAYKORAWIIPPFYCQIFDPALMLVAI	120
b	b	121	TVLIYPNSIQCYIROLPPNFPYRDDWMSVNPTCLVILFLFISIILTFKGYLISCVWNCY	180
b	b	121	TVLIYPNSIQCYIROLPPNFPYRDDWMSVNPTCLVILFLFISIILTFKGYLISCVWNCY	180
b	b	181	RYINGRNSSDVLYVYTSNDTIVLIPPYDDATNGAAKEPPPPYVSA	226
b	b	181	RYINGRNSSDVLYVYTSNDTIVLIPPYDDATNGAAKEPPPPYVSA	226
		RESULT 5		
D	AAB88317	standard; Protein;	226 AA.	
C	AAB88317;			
X		23-MAY-2001	(first entry)	
				Human membrane or secretory protein clone PSEC001.
				Human. Secretory protein: membrane protein; vaccine; gene therapy.
Qy		1	MKQVAPWTRFYSNSCUCCHVRGTTILGWYVILINAVVLLISALADPQDNFSSSEL	60
Db		1	MKQVAPWTRFYSNSCUCCHVRGTTILGWYVILINAVVLLISALADPQDNFSSSEL	60
Qy		61	GGDPEFDANMCIAISLMLILICATYGAJKORAWIIPPFYCQLFDFALMLVAI	120
Db		61	GGDPEFDANMCIAISLMLILICATYGAJKORAWIIPPFYCQIFDFALMLVAI	120
Qy		121	TWLIYPNSIQCYIROLPPNFPYRDDWMSVNPTCLVILFLFISIILTFKGYLISCVWNCY	180
Db		121	TWLIYPNSIQCYIROLPPNFPYRDDWMSVNPTCLVILFLFISIILTFKGYLISCVWNCY	180
Qy		181	RYINGRNSSDVLYVYTSNDTIVLIPPYDDATNGAAKEPPPPYVSA	226
Db		181	RYINGRNSSDVLYVYTSNDTIVLIPPYDDATNGAAKEPPPPYVSA	226

WPI: 2001-093989/11.
N-PSDB; AAF93744.

X Nucleic acids encoding secretory proteins/membrane proteins, useful in
T gene therapy or as candidate target molecules in drug development -
T gene therapy or as candidate target molecules in drug development -
S Claim 1; SEQ ID 2; 60pp + CD ROM; English.

X This invention relates to nucleic acid sequences AAF93744 - AAF93916
C which encode human secretory or membrane proteins represented by
C AAB88171 - AAF88419. Included in the invention are primers
C AAF94295 and AAF62232 - AAF62235 which are used to isolate the
C cDNA sequences of the invention. The invention also includes methods for
C the production of antibodies directed against the proteins, and cDNA
C sequences, which can be used in vaccines. The nucleic acid sequences

XX Novel 1405 isolated polypeptides, useful for diagnosis, treatment and prevention of neural, immune system, muscular, reproductive, PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders -

XX Claim 11; SEQ ID NO 1994; 2081pp + Sequence Listing; English.

XX The invention relates to novel genes (ABL89449-ABU90853) and proteins (ABU9040-ABB9044) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (anti)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 226 AA;

Query Match 100.0%; Score 1200; DB 23; Length 226;

Best Local Similarity 100.0%; Pred. No. 2.4e-125; Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRMVAWPTRFSNSCLCCHVTRGTLGWLILNAVLLILSALDDQXNFSSSEL 60

Db 1 MRMVAWPTRFSNSCLCCHVTRGTLGWLILNAVLLILSALDDQXNFSSSEL 60

Qy 61 GGDPEMDAMCIAIAISLMLICAMATYGAJKORAMIIIPFRCYQIDDFALNMLVAI 120

Db 61 GGDPEMDAMCIAIAISLMLICAMATYGAJKORAMIIIPFRCYQIDDFALNMLVAI 120

Qy 121 TVLIYNSIQBYIQLPNNPYRDDMSNPTCLVLLIIFISILTFKGYLISCVWNCY 180

Db 121 TVLIYNSIQBYIQLPNNPYRDDMSNPTCLVLLIIFISILTFKGYLISCVWNCY 180

Qy 181 RYINGRNSSDVLYVYTISNDTIVLLPPYDATVNGAAKEPPPYVSA 226

Db 181 RYINGRNSSDVLYVYTISNDTIVLLPPYDATVNGAAKEPPPYVSA 226

RESULT 7

ID ABU56591 Standard; Protein; 226 AA.

XX AC ABU56591;

XX DT 02-APR-2003 (first entry)

DE Lung cancer-associated polypeptide #184.

XX KW Lung cancer-associated polypeptide; cyrostatic; emphysema;

KW anti-inflammatory; anti-ashmatic; non-small cell lung cancer; atelectasis;

KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;

KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;

KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.

XX OS Unidentified.

PN WO200286443-A2.

XX PD 31-OCT-2002.

XX PP 18-APR-2002; 2002WO-US12476.

XX PR 18-APR-2001; 2001US-28470P.
PR 10-MAY-2001; 2001US-290492P.
PR 09-NOV-2001; 2001US-33245P.
PR 13-NOV-2001; 2001US-35066P.
PR 29-NOV-2001; 2001US-333370P.
PR 12-APR-2002; 2002US-372246P.
XX PA (EOB-) EOS BIOTECHNOLOGY INC.
XX PI Aziz N, Murray R;
XX DR WPI: 2003-093161/08.
XX N-PSDB; ABX76320.
XX PA Claim 27; Page 327; 453pp; English.
XX The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer-associated polynucleotides and polypeptides are used for identifying a compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer, non-small cell lung cancer or other benign or precancerous lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides and polypeptides are useful as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences ABU56408-ABU56745 represent lung cancer-associated polypeptides of the invention.
XX SQ Sequence 226 AA;
XX Query Match 100.0%; Score 1200; DB 24; Length 226;
XX Best Local Similarity 100.0%; Pred. No. 2.4e-125; Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX Qy 1 MRMVAWPTRFSNSCLCCHVTRGTLGWLILNAVLLILSALDDQXNFSSSEL 60
XX Db 1 MRMVAWPTRFSNSCLCCHVTRGTLGWLILNAVLLILSALDDQXNFSSSEL 60
XX Qy 61 GGDPEMDAMCIAIAISLMLICAMATYGAJKORAMIIIPFRCYQIDDFALNMLVAI 120
XX Db 61 GGDPEMDAMCIAIAISLMLICAMATYGAJKORAMIIIPFRCYQIDDFALNMLVAI 120
XX Qy 121 TVLIYNSIQBYIQLPNNPYRDDMSNPTCLVLLIIFISILTFKGYLISCVWNCY 180
XX Db 121 TVLIYNSIQBYIQLPNNPYRDDMSNPTCLVLLIIFISILTFKGYLISCVWNCY 180
XX Qy 181 RYINGRNSSDVLYVYTISNDTIVLLPPYDATVNGAAKEPPPYVSA 226
XX Db 181 RYINGRNSSDVLYVYTISNDTIVLLPPYDATVNGAAKEPPPYVSA 226
XX Qy 1 MRMVAWPTRFSNSCLCCHVTRGTLGWLILNAVLLILSALDDQXNFSSSEL 60
XX Db 1 MRMVAWPTRFSNSCLCCHVTRGTLGWLILNAVLLILSALDDQXNFSSSEL 60
XX Qy 61 GGDPEMDAMCIAIAISLMLICAMATYGAJKORAMIIIPFRCYQIDDFALNMLVAI 120
XX Db 61 GGDPEMDAMCIAIAISLMLICAMATYGAJKORAMIIIPFRCYQIDDFALNMLVAI 120
XX Qy 121 TVLIYNSIQBYIQLPNNPYRDDMSNPTCLVLLIIFISILTFKGYLISCVWNCY 180
XX Db 121 TVLIYNSIQBYIQLPNNPYRDDMSNPTCLVLLIIFISILTFKGYLISCVWNCY 180
XX Qy 181 RYINGRNSSDVLYVYTISNDTIVLLPPYDATVNGAAKEPPPYVSA 226
XX Db 181 RYINGRNSSDVLYVYTISNDTIVLLPPYDATVNGAAKEPPPYVSA 226
XX Qy 1 MRMVAWPTRFSNSCLCCHVTRGTLGWLILNAVLLILSALDDQXNFSSSEL 60
XX Db 1 MRMVAWPTRFSNSCLCCHVTRGTLGWLILNAVLLILSALDDQXNFSSSEL 60
XX Qy 121 TVLIYNSIQBYIQLPNNPYRDDMSNPTCLVLLIIFISILTFKGYLISCVWNCY 180
XX Db 121 TVLIYNSIQBYIQLPNNPYRDDMSNPTCLVLLIIFISILTFKGYLISCVWNCY 180
XX Qy 181 RYINGRNSSDVLYVYTISNDTIVLLPPYDATVNGAAKEPPPYVSA 226
XX Db 181 RYINGRNSSDVLYVYTISNDTIVLLPPYDATVNGAAKEPPPYVSA 226
XX OS Unidentified.
XX ID AAM41361 Standard; Protein; 231 AA.
XX AC AAM41361;
XX DT 22-OCT-2001 (first entry)
XX RESULT 8
XX AAM41361
XX ID AAM41361
XX AC AAM41361;
XX DT 22-OCT-2001
XX PP

DE	Human polypeptide SEQ ID NO 6292.	Db	126 TVLIYPNSIQEYIRQLPPNFPYRDDVMSVNPCTCLVLLILFISILITPKGYLISCVWNY 185
XX	Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;	Qy	181 RYINGRNSSDVLYVTTSNDTTVLPPYDATTNGAAKERPPPYSA 226
XX	peripheral nervous system; neuropathy; central nervous system; CNS;	Db	186 RYINGRNSSDVLYVTTSNDTTVLPPYDATTNGAAKERPPPYSA 231
XX	Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;		
XX	amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;		
XX	chemokinetic; thrombolytic; drug screening; arthritis; inflammation;		
XX	leukaemia.		
OS	Homo sapiens.	RESULT 9	
XX		ID ABP64704	ABP64704 standard; Protein; 283 AA.
XX		ID XX	
PN	WO200153312-A1.	AC XX	
XX		ABP64704;	
PD	26-JUL-2001.	DT XX	
XX		25-FEB-2003 (first entry)	
PF	26-DEC-2000; 2000WO-US34263.	XX	Human protein SEQ ID 364.
XX		DB XX	
PR	21-JAN-2000; 2000US-0488725.	XX	Human; expressed sequence tag; EST;
PR	25-APR-2000; 2000US-0552317.	XX	haematopoietic disorder; central nervous system disease; viral infection;
PR	09-JUL-2000; 2000US-059804.	XX	peripheral nervous system disease; non-healing wound; infectious disease;
PR	19-JUL-2000; 2000US-062012.	XX	immune deficiency; immune disorder; bacterial infection; allergy; cancer;
PR	03-AUG-2000; 2000US-0653450.	XX	fungal infection; autoimmune disorder; coagulation disorder; nootropic;
PR	14-SEP-2000; 2000US-0662191.	XX	anti-allergic; anti-inflammatory; immunosuppressive; neuroprotective;
PR	19-OCT-2000; 2000US-0693036.	XX	cytostatic; haemostatic; viricide; antibacterial; fungicide;
PR	29-NOV-2000; 2000US-0727344.	XX	immunostimulant; cerebroprotective.
XX		OS Homo sapiens.	
PA	(HYSE-) HYSEQ INC.	XX	
XX	Tang YT, Liu C, Abundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;	PN WO200259260-A2.	
PI	PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;	XX	
PI	PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;	PD 01-AUG-2002.	
XX		XX	
DR	WPI; 2001-442253/47.	PP 16-NOV-2001; 2001WO-US42950.	
DR	N-PSDB; WPI60517.	PR 17-NOV-2000; 2000US-0714936.	
XX		XX	
PT	Novel nucleic acids and polypeptides, useful for treating disorders	(HYSE-) HYSEQ INC.	
PT	such as central nervous system injuries -	XX	
PS	Example 2; SEQ ID NO 6292; 10078pp; English.	PI Tang YT, Goodrich RW, Liu C, Zhou P, Abundi V, Wehrman T, Drmanac RT;	
XX		PI Ren F, Xue AJ, Yang Y, Wehrman T, Drmanac RT;	
CC	The invention relates to human nucleic acids (AAI57798 AAI61369) and	XX	
CC	the encoded polypeptides (AMM8642 AMM4213) with nootropic,	XX	
CC	immuno-suppressant and cytostatic activity. The polynucleotides are useful	XX	
CC	in gene therapy. A composition containing a polypeptide or polynucleotide	XX	
CC	of the invention may be used to treat diseases of the peripheral nervous	XX	
CC	system, such as peripheral nervous injuries, peripheral neuropathy and	XX	
CC	localised neuropathies and central nervous system diseases, such as	XX	
CC	Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic	XX	
CC	lateral sclerosis, and Shy-Drager Syndrome. Other uses include the	XX	
CC	utilisation of the activities such as: Immune system suppression,	XX	
CC	Activ/inhibin activity, chemotactic/chemokinetic activity, haemostatic	CC	
CC	and thrombolytic activity, cancer diagnosis and therapy, drug screening,	CC	
CC	assays for receptor activity, arthritis and inflammation, leukaemias and	CC	
CC	C.N.S disorders.	CC	
CC	Note: The sequence data for this patent did not form part of the printed	CC	
CC	specification.	CC	
XX	Sequence 231 AA;	CC	
Qy	Query Match 100.0%; Score 1200; DB 22; Length 231;	CC	
	Best Local Similarity 100.0%; Pred. No. 2.4e-125;	CC	
	Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	CC	
Db	1 MRKVAPTRPYSNSCCCLCHYRTGTLGWWYLILSADPQYNSSSL 60	CC	
Db	6 MRKVAPTRPYSNSCCCLCHYRTGTLGWWYLILSADPQYNSSSL 65	CC	
Qy	61 GGDDEBENDDANCIATIAISLMLILICAMATYGAYKORAWIIPFFCYQIFDFALNLVAI 120	CC	
Db	66 GGDDEPFDNDANCIATIAISLMLILICAMATYGAYKORAWIIPFFCYQIFDFALNLVAI 125	CC	
Qy	121 TVLIYPNSIQEYIRQLPPNFPYRDDVMSVNPCTCLVLLPISIILTPKGYLISCVWNY 180	CC	

Page 7

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp://wipo.int/patdb/pct/sequences](http://wipo.int/patdb/pct/sequences).

from a non cancer patient - Disclosure; Page 296-297; 481pp; English.

XX 16-APR-2001; 2001WO-US08656.
 PF
 XX 18-APR-2000; 2000US-0552929.
 PR 26-JAN-2001; 2001US-0770160.
 XX (HYSEQ-) HYSEQ INC.
 PA

PI Tang YT, Liu C, Drmanac RT;
 XX DR, 2001-611725/70.
 XX PT
 PT Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -
 XX PS Claim 20; Page 283; 765pp; English.
 XX The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and they can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate hematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemia. AAU29510-AAU3304 represent the amino acid sequences of novel human secreted proteins of the invention.

XX SQ Sequence 301 AA; Score 74.4%; Best Local Similarity 77.9%; Pred. No. 6.4e-91; Matches 176; Conservative 7; Mismatches 40; Indels 3; Gaps 3;

Qy 1 MRMVAPWTRFYSNSCLCCHVRGTGTLGGWYLINAVVLLILSAL-ADPDQYNSSE 59
 Db 70 MKMVAPWTRFYSNSCLCCHVRGTGTLGGWYLINAVVLYDFIECPGXSQSSITFQVLE 129

Qy 60 LGGDFEFMDANM-CIAIAISLMLICAVATGYAKQRAWIIPFFCQIFDPALNNY 118
 Db 130 LGGDFEFMDANNGAFIAISLMLICAVATGYAKQRAWIIPFFCQIFDPALTCV 189

Qy 119 ATIVLIPYNSQEYTRQLPPNPFYRDDVMSVNPCTLVILFISILTFKGYLISCVNN 178
 Db 190 AISGLIYANSQENTRELPPKFYPPNDAMSVNPTCLVFLFILFISILTFKGYLISCVNN 249

Qy 179 CYRYINGRNSDVLYVVTNSNDT-TVLLPYDDATYNGAAKEPPPPY 223
 Db 250 CYRYINGRNSAXCPWFMPLPAMTLRCYPPTDDATYNGAAKEPPPPY 295

Query Match Score 892.5; DB 22; Length 301;
 Best Local Similarity 77.9%; Pred. No. 6.4e-91;
 Matches 176; Conservative 7; Mismatches 40; Indels 3; Gaps 3;

Qy 1 MRMVAPWTRFYSNSCLCCHVRGTGTLGGWYLINAVVLLILSAL-ADPDQYNSSE 59
 Db 70 MKMVAPWTRFYSNSCLCCHVRGTGTLGGWYLINAVVLYDFIECPGXSQSSITFQVLE 129

Qy 60 LGGDFEFMDANM-CIAIAISLMLICAVATGYAKQRAWIIPFFCQIFDPALNNY 118
 Db 130 LGGDFEFMDANNGAFIAISLMLICAVATGYAKQRAWIIPFFCQIFDPALTCV 189

Qy 119 ATIVLIPYNSQEYTRQLPPNPFYRDDVMSVNPCTLVILFISILTFKGYLISCVNN 178
 Db 190 AISGLIYANSQENTRELPPKFYPPNDAMSVNPTCLVFLFILFISILTFKGYLISCVNN 249

Qy 179 CYRYINGRNSDVLYVVTNSNDT-TVLLPYDDATYNGAAKEPPPPY 223
 Db 250 CYRYINGRNSAXCPWFMPLPAMTLRCYPPTDDATYNGAAKEPPPPY 295

RESULT 12
 AAE25970 standard; Protein; 162 AA.
 ID AAE26970 first entry
 DE Human gene 12 encoded secreted protein HTEBY84, SEQ ID NO:63.
 XX AC AAE26970;
 XX 13-DEC-2002 (first entry)
 XX Human; immunodeficiency; X-linked agammaglobulinaemia; septic shock;
 XX autoimmune disorder; rheumatoid arthritis; multiple sclerosis; cancer;
 KW Graves' disease; diabetes mellitus; haematoopoietic disorder; stroke;
 KW respiratory disorder; asthma; allergy; gastrointestinal disorder;
 KW inflammatory bowel disease; neurodegenerative disorder; hepatitis;

KW Parkinson's disease; Alzheimer's disease; cardiovascular disorder;
 KW atherosclerosis; myocarditis; renal disorder; fungicide; viricide;
 KW hyperproliferative disorder; acute glomerulonephritis; tonsillitis;
 KW respiratory disorder; rhinitis; sinusitis; neurological disease;
 KW endocrine disorder; Addison's disease; reproductive system disorder;
 KW endometriosis; vasotropin; voluntary; cytostatic; nortropic; cardiot;
 KW anti-HIV; tranquilliser; gout; antiparasitic.
 XX OS Homo sapiens.
 XX PR 11-MAY-2001; 2001US-0852659.
 XX PR 11-SEP-1998; 98US-0152060.
 XX PR 20-JUN-2002.
 XX PF XX
 XX PA (RUBE/); RUBEN S M.
 XX PA (ROSE/); ROSEN C A.
 XX PA (LIXY/); LI Y.
 XX PA (ZENG/); ZENG Z.
 XX PA (KYAW/); KYAW H.
 XX PA (FISCH/); FISCHER C L.
 XX PA (LJHH/); LI H.
 XX PA (SOPP/); SOPPET D R.
 XX PA (GENT/); GENTZ R L.
 XX PA (WEY/); WEI Y.
 XX PI Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
 XX PI Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
 XX PI Perrie AM;
 XX DR WPI; 2002-590780/64.
 XX DR N-PSDB; AAD44647.
 XX PT Novel human secreted polypeptides and polynucleotides for diagnosing, preventing, treating immune, hyperproliferative, cardiovascular, neurological, reproductive disorders and identifying modulators of therapeutic use -
 XX PS Claim 11; Page 178; 209pp; English.
 XX CC AAD4636-AAD4676 represent cDNAs corresponding to 28 human secreted protein genes, and AAE6959-AAE26999 represent the proteins they encode.
 XX CC AAE7000-AAE2025 represent human secreted protein fragments or their variants. The secreted proteins and genes are useful for preventing, therapy. Specific uses are described for each of the 28 genes, based on the tissues in which they are most highly expressed and include developing products for the diagnosis or treatment of immunodeficiencies, e.g., X-linked agammaglobulinaemia, B cell immunodeficiencies, severe combined immunodeficiencies, autoimmune disorders e.g., systemic lupus erythematosus, rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis, autoimmune haemolytic anaemia, Goodpasture's syndrome, Grave's disease, diabetes mellitus, dermatitis, inflammatory conditions including septic shock, sepsis, reperfusion injury, inflammatory bowel disease, Crohn's disease, hematopoietic disorders, respiratory disorders e.g., asthma and allergy, gastrointestinal disorders e.g., inflammatory bowel disease), cancers e.g., gastric, ovarian, lung, pancreatic, sarcomas and allogenic transplant rejection, blood-related disorder (thrombosis, arterial thrombosis, atherosclerosis), ischaemic brain injury and/or stroke, neurodegenerative disorders e.g., Parkinson's disease and Alzheimer's disease, AIDS-related dementia and prion disease, cardiovascular disorders e.g., hepatitis, gout, trauma, ischaemic, brain injury and/or stroke, respiratory disorders e.g., rhinitis, sinusitis, tonsillitis, lung cancer, allergic disorders, pneumonitis, bronchitis, cardiosclerosis, inflammatory disorders e.g., hepatitis, atherosclerosis, sarcoidosis and allogenic transplant rejection, blood-related disorder (thrombosis, arterial thrombosis, atherosclerosis), ischaemic brain injury and/or stroke, neurodegenerative disorders e.g., rhinitis, sinusitis, tonsillitis, liver cancer, hepatitis, ovarian, lung, renal disorders e.g., acute glomerulonephritis, neurological diseases, liver disorders, endocrine disorders e.g., hyperthyroidism, Addison's disease, hypopituitarism, infectious diseases and reproductive system disorders e.g., endometriosis. The present sequence represents a human

CC secreted protein of the invention.
 XX SQ Sequence 162 AA;

Query Match 64.1%; Score 769; DB 23; Length 162;

Best Local Similarity 99.3%; Pred. No. 1.7e-77; Matches 146; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX Qy 1 MKWVAPTPRFPSNSCCCLCHYVRTGTLGQWYLINAVVLLILLSSALADPQYNFSSSEL 60

Db 1 MKWVAPTPRFPSNSCCCLCHYVRTGTLGQWYLINAVVLLILLSSALADPQYNFSSSEL 60

Qy 61 GGDFFBFDMDANNCIAIAISLUMILICAMATGAYKORAGTIPFFCYQIDFDALNLVAI 120

Db 61 GGDFFBFDMDANNCIAIAISLUMILICAMATGAYKORAGTIPFFCYQIDFDALNLVAI 120

Qy 121 TVLIYPNSIQEXIROLPPNPYRDDW 147

Db 121 TVLIYPNSIQEXIROLPPNPYRDDW 147

RESUIT 13
 AAE27108 AA
 ID AAE27108 standard; Protein; 162 AA.

XX AC AAE27108;

XX DT 13-DEC-2002 (first entry)

XX DB Human gene 12 encoded secreted protein HTEBY84, SEQ ID NO:63.

XX Human; secreted protein; autoimmune disease; hyperproliferative disorder; rheumatoid arthritis; neoplasm; cerebrovascular disorder; angiogenesis; cerebral ischaemia; cardiovascular disorder; nervous system disorder; cardiac arrest; Alzheimer's disease; ocular disorder; wound healing; infection; corneal infection; skin aging; food additive; preservative; tissue regeneration; immunosuppressive; antiproliferative; cytostatic; cardiotonic; vasoroplastic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucidal; fungicide; ophthalmological; gene therapy; pulmonary.
 XX Homo sapiens.
 PN US2002076756-A1.
 XX PD 20-JUN-2002.
 XX PP 11-MAY-2001; 2001US-0853161.
 XX PR 02-FEB-2001; 2001US-265583P.

XX PA (RUBE/) RUBEN S M.
 PA (ROSE/) ROSEN C A.
 PA (LIY/) LI Y.
 PA (ZENG/) ZENG Z.
 PA (KYAW/) KYAW H.
 PA (FISC/) FISCHER C L.
 PA (LIHH/) LI H.
 PA (SOPP/) SOPPET D R.
 PA (GENT/) GENTZ R L.
 PA (WEI/) WEI Y.
 PA (MOOR/) MOORE P A.
 PA (YOUN/) YOUNG P E.
 PA (GREEN/) GREENE J M.
 PA (FERR/) FERRIE A M.
 XX PI Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
 PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
 PI Ferrie AM;
 DR WPI: 2002-574454/61.
 DR N-PSDB; AAD44865.

CC New nucleic acid molecules encoding 28 human secreted proteins, useful for diagnosing, preventing, treating or ameliorating medical conditions and as food additives or preservatives -

XX PS Claim 11; Page 178; 209pp; English.

XX AAD44854-AAD44984 represent cDNAs corresponding to 28 human secreted protein genes, and AAE27097-AAE27137 represent the proteins they encode.

CC CC and their corresponding secreted proteins are useful for preventing, CC CC treating or ameliorating medical conditions, e.g., by protein or gene CC therapy. Secreted protein sequences of the invention are useful for the CC diagnosis or treatment of disorders such as autoimmune diseases (e.g., CC rheumatoid arthritis), hyperproliferative disorders (e.g., neoplasms of CC the breast or liver), cerebrovascular disorders (e.g., cerebral ischaemia, CC angiogenesis), cardiovascular disorders (e.g., cardiac arrest), nervous CC system disorders (e.g., Alzheimer's disease), infections caused by fungi, CC bacteria and viruses and ocular disorders (e.g., corneal infection). The CC polypeptides can also be used to aid wound healing and epithelial cell CC proliferation, to prevent skin aging due to sunburn, to maintain organs CC before transplantation, for supporting cell culture of primary tissues, CC to regenerate tissues and in chemotaxis. They can also be used as food CC additives or preservative to increase or decrease storage capabilities, CC fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors CC and other nutritional components. The present sequence represents a human CC secreted protein of the invention.

XX SQ Sequence 162 AA;

Query Match 64.1%; Score 769; DB 23; Length 162;
 Best Local Similarity 99.3%; Pred. No. 1.7e-77; Matches 146; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKWVAPTPRFPSNSCCCLCHYVRTGTLGQWYLINAVVLLILLSSALADPQYNFSSSEL 60

Db 1 MKWVAPTPRFPSNSCCCLCHYVRTGTLGQWYLINAVVLLILLSSALADPQYNFSSSEL 60

Qy 61 GGDFFBFDMDANNCIAIAISLUMILICAMATGAYKORAGTIPFFCYQIDFDALNLVAI 120

Db 61 GGDFFBFDMDANNCIAIAISLUMILICAMATGAYKORAGTIPFFCYQIDFDALNLVAI 120

Qy 61 TVLIYPNSIQEXIROLPPNPYRDDW 147

Db 61 TVLIYPNSIQEXIROLPPNPYRDDW 147

Qy 121 TVLIYPNSIQEXIROLPPNPYRDDW 147

Db 121 TVLIYPNSIQEXIROLPPNPYRDDW 147

RESULT 14
 ABU64981 standard; Protein; 162 AA.

ID ABU64981; ABU64981;

XX Human secreted protein gene 12, protein #1.

XX AC ABU64981;

KW Secreted protein; immunodeficiency; multiple sclerosis; severe combined immunodeficiency; autoimmune disorder; cancer; KW rheumatoid arthritis; diabetes mellitus; haematopoietic disorder; inflammatory condition; septic shock; inflammatory bowel disease; Crohn's disease; respiratory disorder; asthma; allergy; stroke; gastrointestinal disorder; central nervous system disorder; ischaemic brain injury; neurodegenerative disorder; Parkinson's disease; Alzheimer's disease; cardiovascular disorder; atherosclerosis; blood-related disorder; thrombosis; atherosclerosis; renal disorder; hyperproliferative disorder; acute glomerulonephritis; Addison's disease; endocrine disorder; liver disease; reproductive system disorder; endometriosis; infectious diseases; pancreatic disorder; vaccine; wound repair; lymphatic disorder; angiogenesis; lymphatic disorder; hair loss; body weight; body height; hair colour; human.

XX OS Homo sapiens.

XX DT 15-MAY-2003 (first entry)

XX DE Human secreted protein gene 12, protein #1.

XX AC ABU64981;

KW Secreted protein; immunodeficiency; multiple sclerosis; severe combined immunodeficiency; autoimmune disorder; cancer; KW rheumatoid arthritis; diabetes mellitus; haematopoietic disorder; inflammatory condition; septic shock; inflammatory bowel disease; Crohn's disease; respiratory disorder; asthma; allergy; stroke; gastrointestinal disorder; central nervous system disorder; ischaemic brain injury; neurodegenerative disorder; Parkinson's disease; Alzheimer's disease; cardiovascular disorder; atherosclerosis; blood-related disorder; thrombosis; atherosclerosis; renal disorder; hyperproliferative disorder; acute glomerulonephritis; Addison's disease; endocrine disorder; liver disease; reproductive system disorder; endometriosis; infectious diseases; pancreatic disorder; vaccine; wound repair; lymphatic disorder; angiogenesis; lymphatic disorder; hair loss; body weight; body height; hair colour; human.

XX OS Homo sapiens.

PN US2002172994-A1.
 XX
 PD 21-NOV-2002.
 XX 11-MAY-2001; 2001US-0852797.
 XX
 PR 14-MAR-1997; 97US-040710P.
 PR 14-MAR-1997; 97US-040762P.
 PR 30-MAY-1997; 97US-048100P.
 PR 30-MAY-1997; 97US-048189P.
 PR 30-MAY-1997; 97US-048577P.
 PR 30-MAY-1997; 97US-050934P.
 PR 06-JUN-1997; 97US-048970P.
 PR 05-SEP-1997; 97US-057765P.
 PR 19-DEC-1997; 97US-068368P.
 PR 02-FEB-2001; 2001US-265583P.
 PR 12-MAR-1998; 98WO-US040858.
 PR 11-SEP-1998; 98US-0152060.
 XX
 PA (RUBE¹) RUBEN S M.
 PA (ROSE¹) ROSEN C A.
 PA (LIIV¹) LI Y.
 PA (ZENG¹) ZENG Z.
 PA (KYAW¹) KYAW H.
 PA (FISCH¹) FISCHER C L.
 PA (LIHH¹) LI H.
 PA (SOPP¹) SOPPET D R.
 PA (GENT¹) GENTZ R L.
 PA (WEIY¹) WEI Y.
 PA (MOOR¹) MOORE P A.
 PA (YOUN¹) YOUNG P E.
 PA (GREEN¹) GREENE J M.
 PA (FERR¹) FERRIE A M.
 XX
 PI Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
 PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
 PI Ferrie AM;
 XX
 DR WPI: 2003-310389/30.
 XX
 DR N-PSDB; ABX96979.
 XX
 PT New human secreted polypeptides and polynucleotides for diagnosing,
 PT prognosing, preventing and treating immune, hyperproliferative, liver,
 PT kidney, reproductive disorders and for identifying modulators of
 PT therapeutic use -
 XX
 PS Claim 11; Page 178; 209PP; English.
 XX
 The invention relates to an isolated polypeptide comprising an amino acid
 sequence at least 95% identical to sequence of 28 human secreted
 proteins, their fragment, polypeptide domain, epitope, secreted form,
 variant, allelic variant, or species homologue, or the encoded sequence
 included in ARCC 97921 and 97922. Also included are the encoding
 nucleic acids, recombinant vectors, host cells, antibodies, and genes.
 The proteins and nucleic acids are useful for diagnosing, preventing,
 treating, prognosing or ameliorating a medical condition, e.g.
 immunodeficiencies (e.g. X-linked agammaglobulinaemia, B cell
 immunodeficiencies, severe combined immunodeficiencies), autoimmune
 disorders (e.g. systemic erythematosus, rheumatoid arthritis, multiple
 sclerosis, autoimmune thyroiditis, autoimmune haemolytic anaemia,
 Goodpasture's syndrome, Grave's disease, diabetes mellitus, dermatitis),
 haemopoietic disorders, inflammatory conditions (e.g. septic shock,
 sepsis), reperfusion injury, inflammatory bowel disease, Crohn's disease),
 respiratory disorders (e.g. asthma and allergy), gastrointestinal
 disorders, cancers (e.g. gastric, ovarian, lung, bladder, liver and
 breast), central nervous system (CNS) disorders (e.g. ischaemic brain
 injury and/or stroke, traumatic brain injury), neurodegenerative
 disorders (e.g. Parkinson's disease and Alzheimer's disease, AIDS-related
 dementia, and prion disease), cardiovascular disorders (e.g.
 atherosclerosis, myocarditis, cardiopulmonary bypass complications),
 pancreatic, sarcoidosis, dermatitis, allogenic transplant rejection),
 CC blood-related disorders (thrombosis, arterial thrombosis),

CC hyperproliferative disorders, renal disorders (e.g. acute
 CC glomerulonephritis), endocrine disorders (e.g. Addison's disease,
 CC hypothyroidism, hyperthyroidism), liver diseases and disorders,
 CC reproductive system disorders (e.g. endometriosis), infectious diseases,
 CC and pancreatic disorders. Many other diseases and disorders are listed in
 CC the specification. They also useful as a vaccine adjuvant. Further they
 CC are useful to enhance or inhibit complement mediated cell lysis, for
 CC stimulating wound and tissue repair, angiogenesis, and the repair of
 CC vascular or lymphatic diseases or disorders. They are also useful
 CC to prevent hair loss, to modulate mammalian characteristics such as body
 CC height, weight, hair colour, and to increase or decrease storage
 CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
 CC minerals, cofactors or other nutritional components. The proteins are
 CC also useful for identifying binding partners. The present sequence
 CC represents a secreted protein of the invention.

XX
 SQ Sequence 162 AA;
 SQ Sequence 162 AA;
 Query Match 64.1%; Score 769; DB 24; Length 162;
 Best Local Similarity 99.3%; Pred. No. 1.7e-77;
 Matches 146; Conservative 0; Missmatches 1; Indels 0; Gaps 0;

Qy 1 MKMYAPWTRFYSNSCCLCCCHVRGTCILGWYLILNAVYLILSALADPQYNSFSSSEL 60
 Db 1 MKMYAPWTRFYSNSCCLCCCHVRGTCILGWYLILNAVYLILSALADPQYNSFSSSEL 60

Qy 61 GGDPEFMDANMCTIAISLMLILICATATGAYKQRAAWIIPPFYCQIFDFALMLVAI 120
 Db 61 GGDPEFMDANMCTIAISLMLILICATATGAYKQRAAGIIPPFYCQIFDFALMLVAI 120

Qy 121 TVLIYPNSIQEYIRQLPPNFPYRDDVM 147
 Db 121 TVLIYPNSIQEYIRQLPPNFPYRDDVM 147

RESULT 15
 ID AAW75240 Standard; Protein; 137 AA.
 XX
 AAW75240 DT 29-JAN-1999 (first entry)
 XX
 Fragment of human secreted protein encoded by gene 12.
 DE Human sapiens.
 XX
 KW secreted protein; fusion protein; gene therapy; protein therapy;
 KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
 KW developmental abnormality; foetal deficiency; blood; allergy; renal;
 KW immune system; asthama; lymphocytic shock; Alzheimer's disease; restenosis; AIDS;
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
 XX
 KW Human sapiens.
 XX
 WO9840463-A2.
 XX
 PN 17-SEP-1998.
 XX
 PD 12-MAR-1998;
 XX
 PR 19-DEC-1997; 97US-004710.
 PR 14-MAR-1997; 97US-0040762.
 PR 30-MAY-1997; 97US-0048100.
 PR 30-MAY-1997; 97US-0048189.
 PR 30-MAY-1997; 97US-0048357.
 PR 30-MAY-1997; 97US-0050934.
 PR 06-JUN-1997; 97US-0048970.
 PR 05-SEP-1997; 97US-0057765.
 XX
 PA (HUMAN) HUMAN GENOME SCI INC.

XX Perrie AM, Fischer CL, Gentz RL, Greene JM, Kyaw H;
 PI Li H, Li Y, Moore PA, Rosen CA, Ruben SM, Soppet DR;
 PT Wei YP, Young PE, Zeng Z;
 XX WPI; 1998-520811/44.
 DR N-PSDB; AAV34297.

XX Isolated human poly(nucleotide(s) encoding secretory peptide(s) - used to develop products for the diagnosis and treatment of e.g. inflammation, cancers, CNS disorders or immune system disorders

XX Disclosure; Page 14; 201pp; English.

XX This sequence represents a fragment of a secreted human protein encoded by the nucleic acid molecule designated Gene 12 (AAV34297). The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAV34277) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 28 novel genes and their fragments (nucleic acid sequences: AAV34286-V34325; amino acid sequences AAW75196-W75235) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 28 polynucleotides, based on which tissues they are most highly expressed in (see AAV34286 for described uses).

XX Sequence 137 AA;

Query	9	RFYSNSCCLCCHVRGTTILGGWYLINAVVLLILSALLADPQINFSSELGGDFEFD	68
Db	1	RPYNSNSCCLCCHVRGTTILGGWYLINAVVLLILSALLADPQINFSSELGGDFEFD	60
Query	69	DANMCIAATSLMLIICAMATYGAVKQRAAWITIPFCYQIFDFALNMVIAITVLYPNS	128
Db	61	DANMCIAATSLMLIICAMATYGAVKQRAAGIIPFCYQIFDFALNMVIAITVLYPNS	120
Query	129	IQEYIRQLPPNPYRQD	145
Db	121	IQEYIRQLPPNPYRQD	137

XX

Search completed: February 2, 2004, 14:21:52
 Job time : 43 secs

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RESULT 2
 US-09-969-6-0A-26
 ; Sequence 26, Application US/0969680A
 ; Publication No. US20030124649A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LAL, Preeti; YUE, Henry
 ; APPLICANT: TANG, Y.; TOM, BANDMAN, Olga
 ; APPLICANT: BURFORD, Neil; AZIMZAI, Yalda
 ; APPLICANT: BAUGHN, Mariah R.; LU, Dyrung Aina M.
 ; APPLICANT: PATTERSON, Chandra
 ; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
 ; FILE REFERENCE: PF-0731-1 USA
 ; CURRENT APPLICATION NUMBER: US/09/969, 680A
 ; CURRENT FILING DATE: 2001-10-02
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/149, 641
 ; PRIOR FILING DATE: 1999-08-17
 ; PRIOR APPLICATION NUMBER: 60/164, 203
 ; PRIOR FILING DATE: 1999-11-09
 ; OTHER INFORMATION: Incyte ID No. US20030124649A1 2795577CD1
 ; SOFTWARE: PERL Program
 SEQ ID NO 26
 LENGTH: 226
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc_feature
 OTHER INFORMATION: Incyte ID No. US20030124649A1 2795577CD1

Query 61 GGDFFEFMDANMCIAAISLIMILICAMATYGAYKORAATIIPFFCYQIFDFALNMLVAI 120
 Db 61 GGDFFEFMDANMCIAAISLIMILICAMATYGAYKORAATIIPFFCYQIFDFALNMLVAI 120
 Query 121 TVLIYPNSIQEYIROLPPNPFYRDDMSNPTCLVLVLIIFISITLTFKGYLISCVNCY 180
 Db 121 TVLIYPNSIQEYIROLPPNPFYRDDMSNPTCLVLVLIIFISITLTFKGYLISCVNCY 180
 Db 181 RYINGRNSDVLVLYTTSNDDTLLPYPDATVNGAAKEPPPYVSA 226
 Db 181 RYINGRNSDVLVLYTTSNDDTLLPYPDATVNGAAKEPPPYVSA 226

US-10-264-237-1994

RESULT 2
 US-10-264-237-1994
 ; Sequence 26, Application US/0969680A
 ; Publication No. US20030124649A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LAL, Preeti; YUE, Henry
 ; APPLICANT: TANG, Y.; TOM, BANDMAN, Olga
 ; APPLICANT: BURFORD, Neil; AZIMZAI, Yalda
 ; APPLICANT: BAUGHN, Mariah R.; LU, Dyrung Aina M.
 ; APPLICANT: PATTERSON, Chandra
 ; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
 ; FILE REFERENCE: PF-0731-1 USA
 ; CURRENT APPLICATION NUMBER: US/09/969, 680A
 ; CURRENT FILING DATE: 2001-10-02
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/149, 641
 ; PRIOR FILING DATE: 1999-08-17
 ; PRIOR APPLICATION NUMBER: 60/164, 203
 ; PRIOR FILING DATE: 1999-11-09
 ; OTHER INFORMATION: Incyte ID No. US20030124649A1 2795577CD1
 ; SOFTWARE: PERL Program
 SEQ ID NO 26
 LENGTH: 226
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc_feature
 OTHER INFORMATION: Incyte ID No. US20030124649A1 2795577CD1

Query Match 100.0%; Score 1200; DB 12; Length 226;
 Best Local Similarity 100.0%; Pred. No. 1. Se-115;
 Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRMVAPWTFYVNSNCLCCHVRGTGILGWYLINAVVLLISALDDQYNFSSEL 60
 Db 1 MRMVAPWTFYVNSNCLCCHVRGTGILGWYLINAVVLLISALDDQYNFSSEL 60
 Qy 61 GGDFFEFMDANMCIAAISLIMILICAMATYGAYKORAATIIPFFCYQIFDFALNMLVAI 120
 Db 61 GGDFFEFMDANMCIAAISLIMILICAMATYGAYKORAATIIPFFCYQIFDFALNMLVAI 120
 Qy 121 TVLYPNSTOEYIQLPPNPFYRDDMSNPTCLVLVLIIFISITLTFKGYLISCVNCY 180
 Db 121 TVLYPNSTOEYIQLPPNPFYRDDMSNPTCLVLVLIIFISITLTFKGYLISCVNCY 180
 Qy 181 RYINGRNSDVLVLYTTSNDDTLLPYPDATVNGAAKEPPPYVSA 226
 Db 181 RYINGRNSDVLVLYTTSNDDTLLPYPDATVNGAAKEPPPYVSA 226

RESULT 4

US-10-301-822-99
 ; Sequence 99, Application US/10301822
 ; Publication No. US20030148410A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Millennium Pharmaceuticals, Inc.
 ; APPLICANT: Berger, Allison
 ; APPLICANT: Guillmette, Tracy L.
 ; APPLICANT: Kamatkar, Shubhangi
 ; APPLICANT: Schlegel, Robert
 ; APPLICANT: Monahan, John E.
 ; APPLICANT: Thibodeau, Stephen N.
 ; APPLICANT: Burgart, Lawrence J.
 ; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND TREATMENT OF COLON CANCER
 ; FILE REFERENCE: MPMP01-029P2RNM
 ; CURRENT APPLICATION NUMBER: US/10/301, 822
 ; CURRENT FILING DATE: 2002-11-21
 ; PRIOR APPLICATION NUMBER: US 60/339, 971
 ; PRIOR FILING DATE: 2001-12-10
 ; PRIOR APPLICATION NUMBER: US 60/361, 978
 ; PRIOR FILING DATE: 2002-03-05
 ; PRIOR APPLICATION NUMBER: US 60/381, 988
 ; PRIOR FILING DATE: 2002-05-20
 ; NUMBER OF SEQ ID NOS: 228
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 99
 LENGTH: 283
 TYPE: PRT
 ORGANISM: Homo Sapiens
 US-10-301-822-99

RESULT 3
 US-10-264-237-1994
 ; Sequence 1994, Application US/10264237
 ; Publication No. US20040009491A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Birse et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

Qy 1 MKKVAPWTRFYSNSCCCLCHVRGTGTLGWLILNAVLLILSALADDQXNFSSSEL 60
 Db 58 MKKVAPWTRFYSNSCCCLCHVRGTGTLGWLILNAVLLILSALADDQXNFSSSEL 117

Qy 61 GGDFFEMDDANMCIAIAISLMLICAMATGAYKQRAAWIIPPFYCQIFDFALNMLVAI 120
 Db 118 GGDFFEMDDANMCIAIAISLMLICAMATGAYKQRAAWIIPPFYCQIFDFALNMLVAI 177

Qy 121 TVLIPNSIOEYIQLPPNPFYRDDVMSYNPTCLVLLILFISIILTFCYLISCVNCY 180
 Db 178 TVLIPNSIOEYIQLPPNPFYRDDVMSYNPTCLVLLILFISIILTFCYLISCVNCY 237

Qy 121 TVLIPNSISQEVYIQLPPNPFYRDDVMSYNPTCLVLLILFISIILTFCYLISCVNCY 180
 Db 178 TVLIPNSISQEVYIQLPPNPFYRDDVMSYNPTCLVLLILFISIILTFCYLISCVNCY 237

Qy 181 RYINGRNSSDVLYVTSNDTTLPPYDATTNGAAKEPPPYVSA 226
 Db 238 RYINGRNSSDVLYVTSNDTTLPPYDATTNGAAKEPPPYVSA 283

RESULT 6
 US-09-853-161-63
 Sequence 63, Application US/09853161
 ; Patent No. US20030076756A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 28 Human Secreted Proteins
 ; FILE REFERENCE: P2003P3
 ; CURRENT APPLICATION NUMBER: US/09/853,161
 ; CURRENT FILING DATE: 2001-05-11
 ; PRIOR APPLICATION NUMBER: 60/265,583
 ; PRIOR FILING DATE: 2001-02-02
 ; PRIOR APPLICATION NUMBER: 09/152,060
 ; PRIOR FILING DATE: 1998-05-11
 ; PRIOR APPLICATION NUMBER: PCT/US98/04858
 ; PRIOR FILING DATE: 1998-03-12
 ; PRIOR APPLICATION NUMBER: 60/040,762
 ; PRIOR FILING DATE: 1997-03-14
 ; PRIOR APPLICATION NUMBER: 60/040,710
 ; PRIOR FILING DATE: 1997-03-14
 ; PRIOR APPLICATION NUMBER: 60/050,934
 ; PRIOR FILING DATE: 1997-05-30
 ; PRIOR APPLICATION NUMBER: 60/048,100
 ; PRIOR FILING DATE: 1997-05-30
 ; PRIOR APPLICATION NUMBER: 60/048,357
 ; PRIOR FILING DATE: 1997-05-30
 ; PRIOR APPLICATION NUMBER: 60/048,189
 ; PRIOR FILING DATE: 1997-05-30
 ; PRIOR APPLICATION NUMBER: 60/057,765
 ; PRIOR FILING DATE: 1997-09-05
 ; PRIOR APPLICATION NUMBER: 60/048,970
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/068,368
 ; PRIOR FILING DATE: 1997-12-19
 ; NUMBER OF SEQ ID NOS: 118
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 63
 ; LENGTH: 162
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-853-161-63

Query Match 64.1%; Score 769; DB 9; Length 162;
 Best Local Similarity 99.3%; Pred. No. 2.6e-71;
 Matches 146; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKKVAPWTRFYSNSCCCLCHVRGTGTLGWLILNAVLLILSALADDQXNFSSSEL 60
 Db 1 MKKVAPWTRFYSNSCCCLCHVRGTGTLGWLILNAVLLILSALADDQXNFSSSEL 60

Qy 61 GGDFFEMDDANMCIAIAISLMLICAMATGAYKQRAAWIIPPFYCQIFDFALNMLVAI 120
 Db 61 GGDFFEMDDANMCIAIAISLMLICAMATGAYKQRAAWIIPPFYCQIFDFALNMLVAI 120

Qy 121 TVLIPNSIOEYIQLPPNPFYRDDVMSYNPTCLVLLILFISIILTFCYLISCVNCY 147
 Db 121 TVLIPNSISQEVYIQLPPNPFYRDDVMSYNPTCLVLLILFISIILTFCYLISCVNCY 147

RESULT 7

US-09-852-652A-63

Sequence 63, Application US/09852659A

Patent No. US20020077287A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: 28 Human Secreted Proteins

FILE REFERENCE: P203P4

CURRENT APPLICATION NUMBER: US/09/852,659A

CURRENT FILING DATE: 2001-05-11

PRIOR APPLICATION NUMBER: 60/040,762

PRIOR FILING DATE: 2001-02-02

PRIOR APPLICATION NUMBER: 60/049,189

PRIOR FILING DATE: 1998-09-11

PRIOR APPLICATION NUMBER: PCT/US98/04858

PRIOR FILING DATE: 1997-03-12

PRIOR APPLICATION NUMBER: 60/040,762

PRIOR FILING DATE: 1997-03-14

PRIOR APPLICATION NUMBER: 60/040,710

PRIOR FILING DATE: 1997-03-14

PRIOR APPLICATION NUMBER: 60/050,934

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: 60/048,100

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: 60/048,189

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: 60/057,765

PRIOR FILING DATE: 1997-09-05

PRIOR APPLICATION NUMBER: 60/048,970

PRIOR FILING DATE: 1997-06-06

PRIOR APPLICATION NUMBER: 60/068,368

PRIOR FILING DATE: 1997-12-19

NUMBER OF SEQ ID NOS: 118

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 63

LENGTH: 162

TYPE: PRT

ORGANISM: Homo sapiens

US-09-852-797-63

Query Match 64.1%; Score 769; DB 10; Length 162;

Best Local Similarity 99.3%; Pred. No. 2.6e-71; Indels 0; Gaps 0;

Matches 146; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query 1 MKMVAAPWTRFYSNSCCCLCHVRGTGTLGGWYLINAVVLLILSALADPQYNFSSSEL 60

Db 1 MKMVAAPWTRFYSNSCCCLCHVRGTGTLGGWYLINAVVLLILSALADPQYNFSSSEL 60

Qy 1 MKMVAAPWTRFYSNSCCCLCHVRGTGTLGGWYLINAVVLLILSALADPQYNFSSSEL 60

Db 1 MKMVAAPWTRFYSNSCCCLCHVRGTGTLGGWYLINAVVLLILSALADPQYNFSSSEL 60

Qy 61 GGDFFEMDDAMNCIAAISLMLICAMATGAYKORAAWIPEFCYQIFDANLMLVAI 120

Db 61 GGDFFEMDDAMNCIAAISLMLICAMATGAYKORAAWIPEFCYQIFDANLMLVAI 120

Qy 121 TVLIYPNSIQEYIRQLQPFPYRVDVM 147

Db 121 TVLIYPNSIQEYIRQLQPFPYRVDVM 147

RESULT 9

US-09-853-161-97

Sequence 97, Application US/09853161

Patent No. US20020076756A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: 28 Human Secreted Proteins

FILE REFERENCE: P2003P3

CURRENT APPLICATION NUMBER: US/09/853,161

CURRENT FILING DATE: 2001-05-11

PRIOR APPLICATION NUMBER: 60/265,583

PRIOR FILING DATE: 2001-02-02

PRIOR APPLICATION NUMBER: 09/152,060

PRIOR FILING DATE: 1998-09-11

PRIOR APPLICATION NUMBER: PCT/US98/04858

PRIOR FILING DATE: 1998-03-12

PRIOR APPLICATION NUMBER: 60/040,762

PRIOR FILING DATE: 1997-03-14

PRIOR APPLICATION NUMBER: 60/048,100

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: 60/048,357

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: 60/050,934

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: 60/048,189

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: 60/057,765

PRIOR FILING DATE: 1997-09-05

PRIOR APPLICATION NUMBER: 60/048,970

PRIOR FILING DATE: 1997-06-06

PRIOR APPLICATION NUMBER: 60/068,368

PRIOR FILING DATE: 1997-12-19

NUMBER OF SEQ ID NOS: 121

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 63

LENGTH: 162

TYPE: PRT

ORGANISM: Homo sapiens

US-09-852-652A-63

Query Match 64.1%; Score 769; DB 9; Length 162;

Best Local Similarity 99.3%; Pred. No. 2.6e-71; Indels 0; Gaps 0;

Matches 146; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query 1 MKMVAAPWTRFYSNSCCCLCHVRGTGTLGGWYLINAVVLLILSALADPQYNFSSSEL 60

Db 1 MKMVAAPWTRFYSNSCCCLCHVRGTGTLGGWYLINAVVLLILSALADPQYNFSSSEL 60

Qy 1 MKMVAAPWTRFYSNSCCCLCHVRGTGTLGGWYLINAVVLLILSALADPQYNFSSSEL 60

Db 1 MKMVAAPWTRFYSNSCCCLCHVRGTGTLGGWYLINAVVLLILSALADPQYNFSSSEL 60

Qy 61 GGDFFEMDDAMNCIAAISLMLICAMATGAYKORAAWIPEFCYQIFDANLMLVAI 120

Db 61 GGDFFEMDDAMNCIAAISLMLICAMATGAYKORAAWIPEFCYQIFDANLMLVAI 120

Qy 121 TVLIYPNSIQEYIRQLQPFPYRVDVM 147

Db 121 TVLIYPNSIQEYIRQLQPFPYRVDVM 147

RESULT 8

US-09-852-797-63

Sequence 63, Application US/09852797

Patent No. US20020172994A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: 28 Human Secreted Proteins

FILE REFERENCE: P2001P2

CURRENT APPLICATION NUMBER: US/09/852,797

CURRENT FILING DATE: 2001-05-11

PRIOR APPLICATION NUMBER: 60/265,583

PRIOR FILING DATE: 2001-02-02

PRIOR APPLICATION NUMBER: 09/152,060

PRIOR FILING DATE: 1998-09-11

PRIOR APPLICATION NUMBER: PCT/US98/04858

Prior Filing Date: 1997-09-05	Pred. No. 9.7e-66;
Prior Application Number: 60/048, 970	Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Prior Filing Date: 1997-06-06	
Prior Application Number: 60/068, 368	
Prior Filing Date: 1997-12-19	
Number of SEQ ID NOS: 118	
Software: PatentIn Ver. 2.0	
SEQ ID NO: 97	
Length: 137	
Type: PRT	
Organism: Homo sapiens	
US-09-853-161-97	
Query Match 59.5%; Score 714; DB 9; Length 137;	
Best Local Similarity 99.3%; Pred. No. 9.7e-66;	
Matches 136; Conservative 0; Mismatches -1; Indels 0; Gaps 0;	
RESULT 10	
US-09-852-659A-97	
Sequence 97, Application US/09852659A	
Patent No. US20020077287A1	
General Information:	
Applicant: Rosen et al.	
Title of Invention: 28 Human Secreted Proteins	
File Reference: P2003PA	
Current Application Number: US/09/852, 659A	
Current Filing Date: 2001-05-11	
Prior Application Number: 60/265, 583	
Prior Filing Date: 2001-02-02	
Prior Application Number: 09/152, 060	
Prior Filing Date: 1998-09-11	
Prior Application Number: PCT/US98/04858	
Prior Filing Date: 1998-03-12	
Prior Application Number: 60/040, 762	
Prior Filing Date: 1997-03-14	
Prior Application Number: 60/050, 934	
Prior Filing Date: 1997-03-12	
Prior Application Number: 60/040, 762	
Prior Filing Date: 1997-03-14	
Prior Application Number: 60/048, 189	
Prior Filing Date: 1997-05-30	
Prior Application Number: 60/048, 100	
Prior Filing Date: 1997-05-30	
Prior Application Number: 60/048, 357	
Prior Filing Date: 1997-05-30	
Prior Application Number: 60/048, 189	
Prior Filing Date: 1997-05-30	
Prior Application Number: 60/057, 765	
Prior Filing Date: 1997-05-30	
Prior Application Number: 60/048, 970	
Prior Filing Date: 1997-06-06	
Prior Application Number: 60/068, 368	
Prior Filing Date: 1997-12-19	
Number of SEQ ID NOS: 118	
Software: PatentIn Ver. 2.0	
SEQ ID NO: 97	
Length: 137	
Type: PRT	
Organism: Homo sapiens	
US-09-852-659A-97	
Query Match 59.5%; Score 714; DB 10; Length 137;	
Best Local Similarity 99.3%; Pred. No. 9.7e-66;	
Matches 136; Conservative 0; Mismatches -1; Indels 0; Gaps 0;	
RESULT 11	
US-09-852-797-97	
Sequence 97, Application US/09852797	
Patent No. US20020172994A1	
General Information:	
Applicant: Rosen et al.	
Title of Invention: 28 Human Secreted Proteins	
File Reference: P2003P2	
Current Application Number: US/09/852, 797	
Current Filing Date: 2001-05-11	
Prior Application Number: 60/265, 583	
Prior Filing Date: 2001-02-02	
Prior Application Number: 09/152, 060	
Prior Filing Date: 1998-03-11	
Prior Application Number: PCT/US98/04858	
Prior Filing Date: 1998-03-12	
Prior Application Number: 60/040, 710	
Prior Filing Date: 1997-03-14	
Prior Application Number: 60/050, 934	
Prior Filing Date: 1997-03-12	
Prior Application Number: 60/040, 762	
Prior Filing Date: 1997-03-14	
Prior Application Number: 60/048, 189	
Prior Filing Date: 1997-05-30	
Prior Application Number: 60/048, 100	
Prior Filing Date: 1997-05-30	
Prior Application Number: 60/048, 357	
Prior Filing Date: 1997-05-30	
Prior Application Number: 60/048, 189	
Prior Filing Date: 1997-05-30	
Prior Application Number: 60/057, 765	
Prior Filing Date: 1997-05-30	
Prior Application Number: 60/048, 970	
Prior Filing Date: 1997-06-06	
Prior Application Number: 60/068, 368	
Prior Filing Date: 1997-12-19	
Number of SEQ ID NOS: 118	
Software: PatentIn Ver. 2.0	
SEQ ID NO: 97	
Length: 137	
Type: PRT	
Organism: Homo sapiens	
US-09-852-659A-97	
Query Match 59.5%; Score 714; DB 9; Length 137;	
Best Local Similarity 99.3%; Pred. No. 9.7e-66;	
Matches 136; Conservative 0; Mismatches -1; Indels 0; Gaps 0;	
RESULT 12	
US-09-852-797-97	
Sequence 97, Application US/09852797	
Patent No. US20020172994A1	
General Information:	
Applicant: Rosen et al.	
Title of Invention: 28 Human Secreted Proteins	
File Reference: P2003P2	
Current Application Number: US/09/852, 797	
Current Filing Date: 2001-05-11	
Prior Application Number: 60/265, 583	
Prior Filing Date: 2001-02-02	
Prior Application Number: 09/152, 060	
Prior Filing Date: 1998-09-11	
Prior Application Number: PCT/US98/04858	
Prior Filing Date: 1998-03-12	
Prior Application Number: 60/040, 762	
Prior Filing Date: 1997-03-14	
Prior Application Number: 60/048, 100	
Prior Filing Date: 1997-05-30	
Prior Application Number: 60/057, 765	
Prior Filing Date: 1997-05-30	
Prior Application Number: 60/048, 357	
Prior Filing Date: 1997-05-30	
Prior Application Number: 60/048, 189	
Prior Filing Date: 1997-05-30	
Prior Application Number: 60/048, 100	
Prior Filing Date: 1997-05-30	
Prior Application Number: 60/057, 765	
Prior Filing Date: 1997-05-30	
Prior Application Number: 60/048, 970	
Prior Filing Date: 1997-06-06	
Prior Application Number: 60/068, 368	
Prior Filing Date: 1997-12-19	
Number of SEQ ID NOS: 121	
Software: PatentIn Ver. 2.0	
SEQ ID NO: 97	
Length: 137	
Type: PRT	
Organism: Homo sapiens	
US-09-852-659A-97	
Query Match 59.5%; Score 714; DB 9; Length 137;	
Best Local Similarity 99.3%; Pred. No. 9.7e-66;	
Matches 136; Conservative 0; Mismatches -1; Indels 0; Gaps 0;	

RESULT 12
 US-10-376-564-12
 ; Sequence 12, Application US/10376564
 ; Publication No. US20030180302A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wolf, Eckhard
 ; APPLICANT: Werner, Sabine
 ; APPLICANT: Halle, Jorn-Peter
 ; APPLICANT: Regenbogen, Johannes
 ; APPLICANT: Goppelt, Andreas
 ; TITLE OF INVENTION: Use of Polypeptides or Nucleic Acids for
 ; the Diagnosis or Treatment of Skin Disorders and Wound
 ; Healing, and for the Identification of Pharmacologically
 ; Active Substances
 ; FILE REFERENCE: 50125/014003
 ; CURRENT APPLICATION NUMBER: US/10/376,564
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIORITY APPLICATION NUMBER: US 09/886,319
 ; PRIORITY FILING DATE: 2001-06-20
 ; PRIORITY FILING DATE: 2000-08-01
 ; PRIORITY FILING DATE: 2000-06-20
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 12
 ; LENGTH: 233
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-376-564-12

Query Match 46.1%; Score 553.5; DB 12; Length 233;
 Best Local Similarity 45.2%; Pred. No. 6.3e-49;
 Matches 104; Conservative 45; Mismatches 60; Indels 21; Gaps 6;
 Qy 9 RFYSNCCCLCHVRGTTILGVWLLINAVVLLILLSALADPD-----QY---NFS 57
 Db 13 RFYSRCCGCCHVRGTTILGVWLLINAVVLLILLSALADPD-----QY---NFS 57
 Qy 58 SELGGDFEFDANMCIAISLMLICAMATGYAKORAANIIPFFCYQIFDFALNL 117
 Db 73 SERMAD-----NACVLEFAVSVLMIISMLVGAISYQVGWLIPFFCYRLFDFVSL 125
 Qy 118 VAITYLIVPNSIQEYIROLPPNPYRDDVMSVNPTCLVILFISILTEFKGLISCW 177
 Db 126 VAISSTLTLPRIKEYLDOL-PDFPKDDIALDSSCLLIVYFFALFIFKAYLINCW 184
 Qy 178 NCYRYINGRNSSDVLY-VTSNDTIVLPPYDDATVNGAAKEPPPYVSA 226
 Db 185 NCYKYINNNRNVPETAVYPAFEAPPQVLPYEMA-VKMPKEKEPPPYLPA 233

RESULT 13
 US-10-264-237-2149
 ; Sequence 13, Application US/10264237
 ; Publication No. US20040009491A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Birse et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PA131P1
 ; CURRENT APPLICATION NUMBER: US/10/264,237
 ; CURRENT FILING DATE: 2001-10-04
 ; PRIORITY APPLICATION NUMBER: PCT/US01/16450
 ; PRIORITY FILING DATE: 2000-05-18
 ; NUMBER OF SEQ ID NOS: 2876
 ; SOFTWARE: PatentIn Ver. 3.1
 ; SEQ ID NO: 2149
 ; LENGTH: 233
 ; TYPE: PRT

Query Match 46.1%; Score 553.5; DB 9; Length 254;
 Best Local Similarity 45.2%; Pred. No. 6.9e-49;
 Matches 104; Conservative 45; Mismatches 60; Indels 21; Gaps 6;
 Qy 9 RFYSNCCCLCHVRGTTILGVWLLINAVVLLILLSALADPD-----QY---NFS 57
 Db 34 RFYSRCCGCCHVRGTTILGVWLLINAVVLLILLSALADPD-----QY---NFS 57
 Qy 58 SELGGDFEFDANMCIAISLMLICAMATGYAKORAANIIPFFCYQIFDFALNL 117
 Db 94 SERMAD-----NACVLEFAVSVLMIISMLVGAISYQVGWLIPFFCYRLFDFVSL 146
 Qy 118 VAITYLIVPNSIQEYIROLPPNPYRDDVMSVNPTCLVILFISILTEFKGLISCW 177
 Db 147 VAISSTLTLPRIKEYLDOL-PDFPKDDIALDSSCLLIVYFFALFIFKAYLINCW 205
 Qy 178 NCYRYINGRNSSDVLY-VTSNDTIVLPPYDDATVNGAAKEPPPYVSA 226
 Db 206 NCYKYINNNRNVPETAVYPAFEAPPQVLPYEMA-VKMPKEKEPPPYLPA 254

RESULT 14
 US-09-925-301-1268
 ; Sequence 14, Application US/09925301
 ; Patent No. US20020052308A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 ; FILE REFERENCE: PA106
 ; CURRENT APPLICATION NUMBER: US/09/925,301
 ; CURRENT FILING DATE: 2001-08-10
 ; PRIORITY APPLICATION NUMBER: PCT/US00/05882
 ; PRIOR FILING DATE: 2000-03-08
 ; PRIOR APPLICATION NUMBER: 60/124,270
 ; PRIOR FILING DATE: 1999-03-12
 ; NUMBER OF SEQ ID NOS: 1634
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 1268
 ; LENGTH: 254
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-925-301-1268

Query Match 46.1%; Score 553.5; DB 9; Length 254;
 Best Local Similarity 45.2%; Pred. No. 6.9e-49;
 Matches 104; Conservative 45; Mismatches 60; Indels 21; Gaps 6;
 Qy 9 RFYSNCCCLCHVRGTTILGVWLLINAVVLLILLSALADPD-----QY---NFS 57
 Db 34 RFYSRCCGCCHVRGTTILGVWLLINAVVLLILLSALADPD-----QY---NFS 57
 Qy 58 SELGGDFEFDANMCIAISLMLICAMATGYAKORAANIIPFFCYQIFDFALNL 117
 Db 94 SERMAD-----NACVLEFAVSVLMIISMLVGAISYQVGWLIPFFCYRLFDFVSL 146
 Qy 118 VAITYLIVPNSIQEYIROLPPNPYRDDVMSVNPTCLVILFISILTEFKGLISCW 177
 Db 147 VAISSTLTLPRIKEYLDOL-PDFPKDDIALDSSCLLIVYFFALFIFKAYLINCW 205
 Qy 178 NCYRYINGRNSSDVLY-VTSNDTIVLPPYDDATVNGAAKEPPPYVSA 226
 Db 206 NCYKYINNNRNVPETAVYPAFEAPPQVLPYEMA-VKMPKEKEPPPYLPA 254

RESULT 15
 US-10-376-564-11
 ; Sequence 15, Application US/10376564
 ; Publication No. US20030180302A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wolf, Eckhard

```

; APPLICANT: Werner, Sabine
; APPLICANT: Halle, Jorn-Peter
; APPLICANT: Regenboogen, Johannes
; APPLICANT: Goppelt, Andreas
; TITLE OF INVENTION: Use of Polypeptides or Nucleic Acids for
; the Diagnosis or Treatment of Skin Disorders and Wound
; TITLE OF INVENTION: Healing and for the Identification of Pharmacologically
; TITLE OF INVENTION: Active Substances
; FILE REFERENCE: 50125/014003
; CURRENT APPLICATION NUMBER: US/10/376,564
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 09/886,319
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 60/222,081
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: DE 100 30 149.5-41
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 11
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-376-564-11

Query Match 45.1%; Score 541.5; DB 12; Length 233;
Best Local Similarity 44.8%; Pred. No. 1.1e-47;
Matches 103; Conservative 44; Mismatches 62; Indels 21; Gaps 6;
; -----
Qy 9 RFYSNSCCLCCHVRYTGTILGWVYLINAVVLLILSALADD-----OY---NFSS 57
Ddb 13 RPYSTRCCGCFHVRYTGTILGTWVNLMAILTVEVTHNSMPAVNQEVGIVNYS 72
; -----
Qy 58 SELGGDEFENDANCMIAIAISLMLICAMATGYKQRAAWIIPPFQIQFDFALNML 117
Ddb 73 SERMAD-----NACVLFAVSVLMEIISLMLVYGGISYQGVWLIFFFCYRLFDPLSCL 125
; -----
Qy 118 VAITVLYIYPNSIQBYTQLPPNFPYRDDMSVNPTLVLVLLFISLTLFKGYLSCVW 177
Ddb 126 VAISSTYLPRIKEYDQL-PDPEYKDDLLADSSCLLPIVVFVVFPIKAYJLNCVW 184
; -----
Qy 178 NCYRYTNGRNSSDVY-VTISNDTTVLPPDDATNGAAKEPPPVYSA 226
Ddb 185 NCYKVNINRNVPETAVYPAFPPTPPQVLPTEBMA-YKIPKECPYLPKA 233

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